

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: ZymoGenetics, Inc.  
1201 Eastlake Avenue East  
Seattle  
WA  
USA  
98102

Anergen, Inc.  
301 Penobscot Drive  
Redwood City  
CA  
USA  
94063

(ii) TITLE OF INVENTION: IMMUNE MEDIATORS AND RELATED METHODS

(iii) NUMBER OF SEQUENCES: 61

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: ZymoGenetics, Inc.  
(B) STREET: 1201 Eastlake Avenue East  
(C) CITY: Seattle  
(D) STATE: WA  
(E) COUNTRY: USA  
(F) ZIP: 98102

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:  
(B) FILING DATE:  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/480,002  
(B) FILING DATE: 07-JUN-1995

200207031301

- (vii) PRIOR APPLICATION DATA:  
 (A) APPLICATION NUMBER: US 08/483,241  
 (B) FILING DATE: 07-JUN-1995

- (vii) PRIOR APPLICATION DATA:  
 (A) APPLICATION NUMBER: US 08/482,133  
 (B) FILING DATE: 07-JUN-1995

- (vii) PRIOR APPLICATION DATA:  
 (A) APPLICATION NUMBER: US 60/005,964  
 (B) FILING DATE: 27-OCT-1995

- (viii) ATTORNEY/AGENT INFORMATION:  
 (A) NAME: Parker, Gary E  
 (B) REGISTRATION NUMBER: 31-648

- (ix) TELECOMMUNICATION INFORMATION:  
 (A) TELEPHONE: 206-442-6673  
 (B) TELEFAX: 206-442-6678

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCGCAAGCTT GAATTCGAGC TCATGGTGTG TCT

33

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

1727	1728	1729	1730	1731	1732	1733	1734	1735	1736	1737	1738	1739	1740	1741	1742	1743	1744	1745	1746	1747	1748	1749	1750	1751	1752	1753	1754	1755	1756	1757	1758	1759	1760	1761	1762	1763	1764	1765	1766	1767	1768	1769	1770	1771	1772	1773	1774	1775	1776	1777	1778	1779	1780	1781	1782	1783	1784	1785	1786	1787	1788	1789	1790	1791	1792	1793	1794	1795	1796	1797	1798	1799	1800	1801	1802	1803	1804	1805	1806	1807	1808	1809	1810	1811	1812	1813	1814	1815	1816	1817	1818	1819	1820	1821	1822	1823	1824	1825	1826	1827	1828	1829	1830	1831	1832	1833	1834	1835	1836	1837	1838	1839	1840	1841	1842	1843	1844	1845	1846	1847	1848	1849	1850	1851	1852	1853	1854	1855	1856	1857	1858	1859	1860	1861	1862	1863	1864	1865	1866	1867	1868	1869	1870	1871	1872	1873	1874	1875	1876	1877	1878	1879	1880	1881	1882	1883	1884	1885	1886	1887	1888	1889	1890	1891	1892	1893	1894	1895	1896	1897	1898	1899	1900	1901	1902	1903	1904	1905	1906	1907	1908	1909	1910	1911	1912	1913	1914	1915	1916	1917	1918	1919	1920	1921	1922	1923	1924	1925	1926	1927	1928	1929	1930	1931	1932	1933	1934	1935	1936	1937	1938	1939	1940	1941	1942	1943	1944	1945	1946	1947	1948	1949	1950	1951	1952	1953	1954	1955	1956	1957	1958	1959	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AATTCGATAT CATGGTGTGT CTGAAGCTCC CTGGAGGCTC CTGCATGACA GCGCTGAC 58

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 58 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CACTGTCAGC GCTGTCATGC AGGAGCCTCC AGGGAGCTTC AGACACACCA TGATATCG 58

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACTTCTTTAA AAACATCGTG ACTCCGCGTA CACCCCGGCC ATCGGGAGGC GGGTCAGGTG 60

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCCACCTG ACCCGCCTCC CGATGGCGGG GGTGTACGCG GAGTCACGAT GTTTTAAAG 60

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGTGACACTG ATGGTGCTGA GCTCCCCACT GGCTTTGTCT GACGAAAACC CAGTAGTGC 59

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGTGACTA CTGGGTTTTTC GTCAGACAAA GCCAGTGGGG AGCTCAGCAC CATCAGTGT 59

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCCGGCTGAT GCTCCCGCT GCACTGT

27

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGCTCTAGA TCATATAGTT GGAGC

25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCAGGGTCTA GATCATAAAG GCCCTGGGTG TCTGGAG

37

(2) INFORMATION FOR SEQ ID NO:11:

bioRxiv preprint doi: <https://doi.org/10.1101/2020.03.11.283000>; this version posted March 11, 2020. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGAGGAATTC GCAGAGACCT CCCAGAGACC AGGATCC

37

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AACACTCTAG ATCACTGCAG GAGCCCTGCT GGAGGAG

37

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGAGGAATTC TGAGTCCTGG TGA CTGCCAT TACCTGT

37

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGAGCATCAG CCGGCATCAA AGAAGAACAT

30

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAGGATGATT AAATGAGTCG CCTCTCGAAG GTGGCTCCAG TGATTAAAGC CAGAATGATG

60

GAGTATGGAA CCACAGGAGG TGGAGGCTCT GGAGGTGGAG GCTCAGGAGG A

111

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single



(ii) MOLECULE TYPE: cDNA

GGAGGCTCAG GAGGAGGTGG GTCCGGAGAC TCCGAAAGG

39

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGCGGGATCC GATCGTGGAG GATGATTAAA TG

32

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCCACCTGAT CCACCCCGCA GGGAGGTGGG

30

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTGGATCAG GTGGCGAAGA CGACATTGAG

30

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCGGAATTCT TAACTAGTAG CTGGGGTGAA

30

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGGAATTCT TAACTAGTAG CTGGGGTGGA

30

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCCACCTGAT CCACCCCGCA GGGAGGTGTG

30

## (2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 107 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CGCGGGATCC GATCGTGGAG GATGATTAAA TGTTCTTTAA AAACATCGTG ACTCCGCGTA

60

CACCCCGCC AGGAGGTGGA GGCTCTGGAG GTGGAGGCTC AGGAGGA

107

## (2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCGGAATTCT TACTTGCTCC GGCAGACTC 30

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GGAGGCTCAG GAGGAGGTGG GTCTGGCGGT GGAGGTCCG GCGGAGGCGG TTCAGAAGAC 60

GACATTGAGG CC 72

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

GGCGGAGGTG GCTCAGGCGG AGGTGGATCT GGAGGTGGAG GCTCAGGCT TGAACAGCCC 60

AAT 63

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 base pairs

(ii) MOLECULE TYPE: cDNA

TGAGCCTCCA CCTCCAGATC CACCTCCGCC TGAGCCACCT CCGCCAGTCT CTGTCAGCTC 60

(2) INFORMATION FOR SEQ ID NO:28:

(ii) MOLECULE TYPE: cDNA

CCGGAATTCT TAACTAGTCT CTGTCAGCTC TGA 33

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Gly Ala Ser Ala Gly

1 5

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 5 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Gly Gly Ser Gly Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 7 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Gly Gly Gly Ser Gly Gly Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:  
    (A) LENGTH: 25 amino acids  
    (B) TYPE: amino acid  
    (C) STRANDEDNESS: single  
    (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser  
20 25

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro Arg  
1 5 10 15

Thr Pro Pro Pro Ser  
20

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gly Gly Ser Gly Gly Gly Gly Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGAGGCTCAG GAGGA  
15

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide



Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala Met  
1 5 10

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 amino acids  
(B) TYPE: amino acid

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Lys Met Phe Pro  
20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 654 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

AGT CGC CTC TCG AAG GTG CCA GTG ATT AAA GCC AGA ATG ATG GAG	48
Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu	
1 5 10 15	
TAT GGA ACC ACA GGA GGT GGA GGC TCT GGA GGT GGA GGC TCA GGA GGA	96
Tyr Gly Thr Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
20 25 30	
GGT GGG TCC GGA GAC TCC GAA AGG CAT TTC GTG CAC CAG TTC AAG GGC	144
Gly Gly Ser Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly	
35 40 45	
GAG TGC TAC TTC ACC AAC GGG ACG CAG CGC ATA CGG CTC GTG ACC AGA	192
Glu Cys Tyr Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg	
50 55 60	
TAC ATC TAC AAC CGG GAG GAG TAC CTG CGC TTC GAC AGC GAC GTG GGC	240
Tyr Ile Tyr Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly	
65 70 75 80	
GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CAC TCA GCC GAG TAC TAC	288
Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr	
85 90 95	
AAT AAG CAG TAC CTG GAG CGA ACG CGG GCC GAG CTG GAC ACG GCG TGC	336
Asn Lys Gln Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys	
100 105 110	
AGA CAC AAC TAC GAG GAG ACG GAG GTC CCC ACC TCC CTG CGG GGT GGA	384
Arg His Asn Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg Gly Gly	
115 120 125	
TCA GGT GGC GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT	432
Ser Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly	
130 135 140	
ACA ACT GTT TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA	480
Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu	
145 150 155 160	

TTT GAT GGT GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT 528  
 Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr  
                   165                  170                  175

GTC TGG AGG CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA 576  
 Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln  
                   180                  185                  190

GGT GGA CTG CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG 624  
 Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu  
                   195                  200                  205

ACT AAG AGG TCA AAT TTC ACC CCA GCT ACT 654  
 Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr  
                   210                  215

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GGA GAC TCC GAA AGG CAT TTC GTG CAC CAG TTC AAG GGC GAG TGC TAC 48  
 Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly Glu Cys Tyr  
   1                  5                  10                  15

TTC ACC AAC GGG ACG CAG CGC ATA CGG CTC GTG ACC AGA TAC ATC TAC 96  
 Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr  
                   20                  25                  30

AAC CGG GAG GAG TAC CTG CGC TTC GAC AGC GAC GTG GGC GAG TAC CGC 144  
 Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg  
                   35                  40                  45

GCG GTG ACC GAG CTG GGG CGG CAC TCA GCC GAG TAC TAC AAT AAG CAG 192  
 Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr Asn Lys Gln  
           50                          55                          60

TAC CTG GAG CGA ACG CGG GCC GAG CTG GAC ACG GCG TGC AGA CAC AAC 240  
 Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys Arg His Asn  
           65                          70                          75                          80

TAC GAG GAG ACG GAG GTC CCC ACC TCC CTG CGG 273  
 Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg  
                                   85                                  90

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT 48  
 Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val  
       1                          5                          10                          15

TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT 96  
 Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly  
                           20                          25                          30

GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG 144  
 Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg  
                           35                          40                          45

CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG 192  
 Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu  
           50                          55                          60

CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG 240  
 Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg  
 65 70 75 80

TCA AAT TTC ACC CCA GCT ACT 261  
 Ser Asn Phe Thr Pro Ala Thr  
 85

## (2) INFORMATION FOR SEQ ID NO:45:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..633

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

TTC TTT AAA AAC ATC GTG ACT CCG CGT ACA CCC CCG CCA GGA GGT GGA 48  
 Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly  
 1 5 10 15

GGC TCT GGA GGT GGA GGC TCA GGA GGA GGT GGG TCC GGA GAC TCC GAA 96  
 Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asp Ser Glu  
 20 25 30

AGG CAT TTC GTG TTC CAG TTC AAG GGC GAG TGC TAC TTC ACC AAC GGG 144  
 Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly  
 35 40 45

ACG CAG CGC ATA CGA TCT GTG GAC AGA TAC ATC TAC AAC CGG GAG GAG 192  
 Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr Asn Arg Glu Glu  
 50 55 60

TAC CTG CGC TTC GAC AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG	240
Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu	
65 70 75 80	
CTG GGG CGG CCA GAC CCC GAG TAC TAC AAT AAG CAG TAC CTG GAG CAA	288
Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Gln	
85 90 95	
ACG CGG GCC GAG CTG GAC ACG GTG TGC AGA CAC AAC TAC GAG GGG GTG	336
Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn Tyr Glu Gly Val	
100 105 110	
GAG ACC CAC ACC TCC CTG CGG GGT GGA TCA GGT GGC GAA GAC GAC ATT	384
Glu Thr His Thr Ser Leu Arg Gly Gly Ser Gly Gly Glu Asp Asp Ile	
115 120 125	
GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA TAT CAG TCT CCT	432
Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro	
130 135 140	
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TGG TTC	480
Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Trp Phe	
145 150 155 160	
TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG CTT CCT GAG TTT	528
Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met Leu Pro Glu Phe	
165 170 175	
GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG CAA AAC ATA GCT	576
Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala	
180 185 190	
ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG TCA AAT TCC ACC	624
Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr	
195 200 205	
CCA GCT ACT	633
Pro Ala Thr	
210	

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GGA GAC TCC GAA AGG CAT TTC GTG TTC CAG TTC AAG GGC GAG TGC TAC	48
Gly Asp Ser Glu Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr	
1 5 10 15	
TTC ACC AAC GGG ACG CAG CGC ATA CGA TCT GTG GAC AGA TAC ATC TAC	96
Phe Thr Asn Gly Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr	
20 25 30	
AAC CGG GAG GAG TAC CTG CGC TTC GAC AGC GAC GTG GGC GAG TAC CGC	144
Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg	
35 40 45	
GCG GTG ACC GAG CTG GGG CGG CCA GAC CCC GAG TAC TAC AAT AAG CAG	192
Ala Val Thr Glu Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln	
50 55 60	
TAC CTG GAG CAA ACG CGG GCC GAG CTG GAC ACG GTG TGC AGA CAC AAC	240
Tyr Leu Glu Gln Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn	
65 70 75 80	
TAC GAG GGG GTG GAG ACC CAC ACC TCC CTG CGG	273
Tyr Glu Gly Val Glu Thr His Thr Ser Leu Arg	
85 90	

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs
- (B) TYPE: nucleic acid



(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA	48
Glu Asp Asp Ile Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val	
1 5 10 15	
TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT	96
Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly	
20 25 30	
GAT GAG TGG TTC TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG	144
Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met	
35 40 45	
CTT CCT GAG TTT GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG	192
Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu	
50 55 60	
CAA AAC ATA GCT ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG	240
Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg	
65 70 75 80	
TCA AAT TCC ACC CCA GCT ACT	261
Ser Asn Ser Thr Pro Ala Thr	
85	

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 16 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CATCGTGGAG GATGAT

16

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAC GAA AAC CCA GTA GTG CAC TTC TTT AAA AAC ATC GTG ACT CCG CGT	48
Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro Arg	
1 5 10 15	
ACA CCC CCG CCA TCG GGA GGC GGG TCA GGT GGA TCC GGG GAC ACC CGA	96
Thr Pro Pro Pro Ser Gly Gly Gly Ser Gly Gly Ser Gly Asp Thr Arg	
20 25 30	
CCA CGT TTC CTG TGG CAG CCT AAG AGG GAG TGT CAT TTC TTC AAT GGG	144
Pro Arg Phe Leu Trp Gln Pro Lys Arg Glu Cys His Phe Phe Asn Gly	
35 40 45	
ACG GAG CGG GTG CGG TTC CTG GAC AGA TAC TTC TAT AAC CAG GAG GAG	192
Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr Asn Gln Glu Glu	
50 55 60	
TCC GTG CGC TTC GAC AGC GAC GTG GGG GAG TTC CGG GCG GTG ACG GAG	240
Ser Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg Ala Val Thr Glu	

"1999-2000" 12-15-00

(2) INFORMATION FOR SEQ ID NO:50:

(A) LENGTH: 279 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..279

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GGG GAC ACC CGA CCA CGT TTC CTG TGG CAG CCT AAG AGG GAG TGT CAT 48  
Gly Asp Thr Arg Pro Arg Phe Leu Trp Gln Pro Lys Arg Glu Cys His  
1 5 10 15

TTC TTC AAT GGG ACG GAG CGG GTG CGG TTC CTG GAC AGA TAC TTC TAT 96  
Phe Phe Asn Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr  
20 25 30

AAC CAG GAG GAG TCC GTG CGC TTC GAC AGC GAC GTG GGG GAG TTC CGG 144  
Asn Gln Glu Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg  
35 40 45

GCG GTG ACG GAG CTG GGG CGG CCT GAC GCT GAG TAC TGG AAC AGC CAG 192  
Ala Val Thr Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln  
50 55 60

AAG GAC ATC CTG GAG CAG GCG CGG GCC GCG GTG GAC ACC TAC TGC AGA 240  
Lys Asp Ile Leu Glu Gln Ala Arg Ala Ala Val Asp Thr Tyr Cys Arg  
65 70 75 80

CAC AAC TAC GGG GTT GTG GAG AGC TTC ACA GTG CAG CGG 279  
His Asn Tyr Gly Val Val Glu Ser Phe Thr Val Gln Arg  
85 90

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

ATC AAA GAA GAA CAT GTG ATC ATC CAG GCC GAG TTC TAT CTG AAT CCT	48
Ile Lys Glu Glu His Val Ile Ile Gln Ala Glu Phe Tyr Leu Asn Pro	
1 5 10 15	
GAC CAA TCA GGC GAA TTT ATG TTT GAC TTT GAT GGT GAT GAG ATT TTC	96
Asp Gln Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp Glu Ile Phe	
20 25 30	
CAT GTG GAT ATG GCA AAG AAG GAG ACG GTC TGG CGG CTT GAA GAA TTT	144
His Val Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe	
35 40 45	
GGA CGA TTT GCC AGC TTT GAG GCT CAA GGT GCA TTG GCC AAC ATA GCT	192
Gly Arg Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala	
50 55 60	
GTG GAC AAA GCC AAC CTG GAA ATC ATG ACA AAG CGC TCC AAC TAT ATG	240
Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Met	
65 70 75 80	
ATC	243
Ile	

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..702

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TTC TTT AAA AAC ATC GTG ACT CCG CGT ACA CCC CCG CCA GGA GGT GGA	48
Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly	
1 5 10 15	
GGC TCT GGA GGT GGA GGC TCA GGA GGA GGT GGG TCT GGC GGT GGA GGT	96
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly	
20 25 30	
TCC GGC GGA GGC GGT TCA GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC	144
Ser Gly Gly Gly Gly Ser Glu Asp Asp Ile Glu Ala Asp His Val Gly	
35 40 45	
GTC TAT GGT ACA ACT GTA TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC	192
Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr	
50 55 60	
ACA CAT GAA TTT GAT GGT GAT GAG TGG TTC TAT GTG GAC TTG GAT AAG	240
Thr His Glu Phe Asp Gly Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys	
65 70 75 80	
AAG GAG ACT ATC TGG ATG CTT CCT GAG TTT GGC CAA TTG ACA AGC TTT	288
Lys Glu Thr Ile Trp Met Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe	
85 90 95	
GAC CCC CAA GGT GGA CTG CAA AAC ATA GCT ACA GGA AAA TAC ACC TTG	336
Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu	
100 105 110	
GGA ATC TTG ACT AAG AGG TCA AAT TCC ACC CCA GCT ACC AAT GAG GCT	384
Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr Pro Ala Thr Asn Glu Ala	
115 120 125	
CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC	432
Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln Pro	
130 135 140	
AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC TTC CCT CCT GTG ATC AAC	480
Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile Asn	
145 150 155 160	
ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG	528

10081294 "000000"

Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr Glu  
                   165                                  170                                  175

ACC AGC TTC CTT GTC AAC CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT 576  
 Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser Tyr  
                   180                                  185                                  190

CTC ACC TTC ATC CCT TCT GAC GAT GAT ATT TAT GAC TGC AAG GTG GAG 624  
 Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu  
                   195                                  200                                  205

CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT 672  
 His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu Ile  
                   210                                  215                                  220

CCA GCC CCC ATG TCA GAG CTG ACA GAG ACT 702  
 Pro Ala Pro Met Ser Glu Leu Thr Glu Thr  
                   225                                  230

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA 48  
 Glu Asp Asp Ile Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val  
   1                                  5                                  10                                  15

TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT 96  
 Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly  
                   20                                  25                                  30

GAT GAG TGG TTC TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG	144
Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met	
35 40 45	
CTT CCT GAG TTT GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG	192
Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu	
50 55 60	
CAA AAC ATA GCT ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG	240
Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg	
65 70 75 80	
TCA AAT TCC ACC CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC	288
Ser Asn Ser Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe	
85 90 95	
CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT	336
Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe	
100 105 110	
GTG GAC AAC ATC TTC CCT CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT	384
Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn	
115 120 125	
AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG ACC AGC TTC CTT GTC AAC	432
Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn	
130 135 140	
CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT	480
Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser	
145 150 155 160	
GAC GAT GAT ATT TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG	528
Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu	
165 170 175	
CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG	576
Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu	
180 185 190	
CTG ACA GAG ACT	588
Leu Thr Glu Thr	
195	



## (2) INFORMATION FOR SEQ ID NO:54:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1323

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

TTC TTT AAA AAC ATC GTG ACT CCG CGT ACA CCC CCG CCA GGA GGT GGA	48
Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly	
1 5 10 15	
GGC TCT GGA GGT GGA GGC TCA GGA GGA GGT GGG TCC GGA GAC TCC GAA	96
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Asp Ser Glu	
20 25 30	
AGG CAT TTC GTG TTC CAG TTC AAG GGC GAG TGC TAC TTC ACC AAC GGG	144
Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly	
35 40 45	
ACG CAG CGC ATA CGA TCT GTG GAC AGA TAC ATC TAC AAC CGG GAG GAG	192
Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr Asn Arg Glu Glu	
50 55 60	
TAC CTG CGC TTC GAC AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG	240
Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu	
65 70 75 80	
CTG GGG CGG CCA GAC CCC GAG TAC TAC AAT AAG CAG TAC CTG GAG CAA	288
Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Gln	
85 90 95	
ACG CGG GCC GAG CTG GAC ACG GTG TGC AGA CAC AAC TAC GAG GGG GTG	336
Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn Tyr Glu Gly Val	

100	105	110	
GAG ACC CAC ACC TCC CTG CGG GGT GGA TCA GGT GGC GAA GAC GAC ATT Glu Thr His Thr Ser Leu Arg Gly Gly Ser Gly Gly Glu Asp Asp Ile 115 120 125			384
GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA TAT CAG TCT CCT Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro 130 135 140			432
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TGG TTC Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Trp Phe 145 150 155 160			480
TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG CTT CCT GAG TTT Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met Leu Pro Glu Phe 165 170 175			528
GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG CAA AAC ATA GCT Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala 180 185 190			576
ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG TCA AAT TCC ACC Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr 195 200 205			624
CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro 210 215 220			672
GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe Val Asp Asn Ile 225 230 235 240			720
TTC CCT CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val 245 250 255			768
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTT GTC AAC CGT GAC CAT TCC Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser 260 265 270			816
TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAC GAT GAT ATT Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile 275 280 285			864

TAT	GAC	TGC	AAG	GTG	GAG	CAC	TGG	GGC	CTG	GAG	GAG	CCG	GTT	CTG	AAA	912
Tyr	Asp	Cys	Lys	Val	Glu	His	Trp	Gly	Leu	Glu	Glu	Pro	Val	Leu	Lys	
290			295			300										
CAT	TGG	GAA	CCT	GAG	ATT	CCA	GCC	CCC	ATG	TCA	GAG	CTG	ACA	GAG	ACT	960
His	Trp	Glu	Pro	Glu	Ile	Pro	Ala	Pro	Met	Ser	Glu	Leu	Thr	Glu	Thr	
305			310			315			320							
GGC	GGA	GGT	GGC	TCA	GGC	GGA	GGT	GGA	TCT	GGA	GGT	GGA	GGC	TCA	CGG	1008
Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Arg	
325			330			335										
CTT	GAA	CAG	CCC	AAT	GTC	GTC	ATC	TCC	CTG	TCC	AGG	ACA	GAG	GCC	CTC	1056
Leu	Glu	Gln	Pro	Asn	Val	Val	Ile	Ser	Leu	Ser	Arg	Thr	Glu	Ala	Leu	
340			345			350										
AAC	CAC	CAC	AAC	ACT	CTG	GTC	TGC	TCA	GTG	ACA	GAT	TTC	TAC	CCA	GCC	1104
Asn	His	His	Asn	Thr	Leu	Val	Cys	Ser	Val	Thr	Asp	Phe	Tyr	Pro	Ala	
355			360			365										
AAG	ATC	AAA	GTG	CGC	TGG	TTC	CGG	AAT	GGC	CAG	GAG	GAG	ACG	GTG	GGG	1152
Lys	Ile	Lys	Val	Arg	Trp	Phe	Arg	Asn	Gly	Gln	Glu	Glu	Thr	Val	Gly	
370			375			380										
GTC	TCA	TCC	ACA	CAG	CTT	ATT	AGG	AAT	GGG	GAC	TGG	ACC	TTC	CAG	GTC	1200
Val	Ser	Ser	Thr	Gln	Leu	Ile	Arg	Asn	Gly	Asp	Trp	Thr	Phe	Gln	Val	
385			390			395			400							
CTG	GTC	ATG	CTG	GAG	ATG	ACC	CCT	CGG	CGG	GGA	GAG	GTC	TAC	ACC	TGC	1248
Leu	Val	Met	Leu	Glu	Met	Thr	Pro	Arg	Arg	Gly	Glu	Val	Tyr	Thr	Cys	
405			410			415										
CAC	GTG	GAG	CAT	CCG	AGC	CTG	AAG	AGC	CCC	ATC	ACT	GTG	GAG	TGG	AGG	1296
His	Val	Glu	His	Pro	Ser	Leu	Lys	Ser	Pro	Ile	Thr	Val	Glu	Trp	Arg	
420			425			430										
GCA	CAG	TCT	GAG	TCT	GCC	CGG	AGC	AAG								1323
Ala	Gln	Ser	Glu	Ser	Ala	Arg	Ser	Lys								
435			440													

## (2) INFORMATION FOR SEQ ID NO:55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..318

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CGG CTT GAA CAG CCC AAT GTC GTC ATC TCC CTG TCC AGG ACA GAG GCC	48
Arg Leu Glu Gln Pro Asn Val Val Ile Ser Leu Ser Arg Thr Glu Ala	
1 5 10 15	
CTC AAC CAC CAC AAC ACT CTG GTC TGC TCA GTG ACA GAT TTC TAC CCA	96
Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro	
20 25 30	
GCC AAG ATC AAA GTG CGC TGG TTC CGG AAT GGC CAG GAG GAG ACG GTG	144
Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val	
35 40 45	
GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC TGG ACC TTC CAG	192
Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln	
50 55 60	
GTC CTG GTC ATG CTG GAG ATG ACC CCT CGG CGG GGA GAG GTC TAC ACC	240
Val Leu Val Met Leu Glu Met Thr Pro Arg Arg Gly Glu Val Tyr Thr	
65 70 75 80	
TGC CAC GTG GAG CAT CCG AGC CTG AAG AGC CCC ATC ACT GTG GAG TGG	288
Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp	
85 90 95	

CGGCTTGAA CAGCCC AATGTC GTCATC TCCCTG TCCAGG ACA GAGGCC 48

318

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1341 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS  
(B) LOCATION: 1..1341

AGT	CGC	CTC	TCG	AAG	GTG	GCT	CCA	GTG	ATT	AAA	GCC	AGA	ATG	ATG	GAG	48
Ser	Arg	Leu	Ser	Lys	Val	Ala	Pro	Val	Ile	Lys	Ala	Arg	Met	Met	Glu	
1				5					10					15		
TAT	GGA	ACC	ACA	GGA	GGT	GGA	GGC	TCT	GGA	GGT	GGA	GGC	TCA	GGA	GGA	96
Tyr	Gly	Thr	Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	
			20					25					30			
GGT	GGG	TCC	GGA	GAC	TCC	GAA	AGG	CAT	TTC	GTG	CAC	CAG	TTC	AAG	GGC	144
Gly	Gly	Ser	Gly	Asp	Ser	Glu	Arg	His	Phe	Val	His	Gln	Phe	Lys	Gly	
		35					40					45				
GAG	TGC	TAC	TTC	ACC	AAC	GGG	ACG	CAG	CGC	ATA	CGG	CTC	GTG	ACC	AGA	192
Glu	Cys	Tyr	Phe	Thr	Asn	Gly	Thr	Gln	Arg	Ile	Arg	Leu	Val	Thr	Arg	
	50					55					60					
TAC	ATC	TAC	AAC	CGG	GAG	GAG	TAC	CTG	CGC	TTC	GAC	AGC	GAC	GTG	GGC	240
Tyr	Ile	Tyr	Asn	Arg	Glu	Glu	Tyr	Leu	Arg	Phe	Asp	Ser	Asp	Val	Gly	
65					70				75					80		

GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CAC TCA GCC GAG TAC TAC Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr	288
85 90 95	
AAT AAG CAG TAC CTG GAG CGA ACG CGG GCC GAG CTG GAC ACG GCG TGC Asn Lys Gln Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys	336
100 105 110	
AGA CAC AAC TAC GAG GAG ACG GAG GTC CCC ACC TCC CTG CGG GGT GGA Arg His Asn Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg Gly Gly	384
115 120 125	
TCA GGT GGC GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT Ser Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly	432
130 135 140	
ACA ACT GTT TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu	480
145 150 155 160	
TTT GAT GGT GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr	528
165 170 175	
GTC TGG AGG CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln	576
180 185 190	
GGT GGA CTG CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu	624
195 200 205	
ACT AAG AGG TCA AAT TTC ACC CCA GCT ACC AAT GAG GCT CCT CAA GCG Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala	672
210 215 220	
ACT GTG TTC CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC AAC ACC CTT Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu	720
225 230 235 240	
ATC TGC TTT GTG GAC AAC ATC TTC CCA CCT GTG ATC AAC ATC ACA TGG Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp	768
245 250 255	
CTC AGA AAT AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG ACC AGC TTC	816

Leu	Arg	Asn	Ser	Lys	Ser	Val	Thr	Asp	Gly	Val	Tyr	Glu	Thr	Ser	Phe		
			260						265							270	
CTC	GTC	AAC	CGT	GAC	CAT	TCC	TTC	CAC	AAG	CTG	TCT	TAT	CTC	ACC	TTC		864
Leu	Val	Asn	Arg	Asp	His	Ser	Phe	His	Lys	Leu	Ser	Tyr	Leu	Thr	Phe		
		275					280					285					
ATC	CCT	TCT	GAT	GAT	GAC	ATT	TAT	GAC	TGC	AAG	GTG	GAG	CAC	TGG	GGC		912
Ile	Pro	Ser	Asp	Asp	Asp	Ile	Tyr	Asp	Cys	Lys	Val	Glu	His	Trp	Gly		
	290					295					300						
CTG	GAG	GAG	CCG	GTT	CTG	AAA	CAC	TGG	GAA	CCT	GAG	ATT	CCA	GCC	CCC		960
Leu	Glu	Glu	Pro	Val	Leu	Lys	His	Trp	Glu	Pro	Glu	Ile	Pro	Ala	Pro		
305					310				315						320		
ATG	TCA	GAG	CTG	ACA	GAG	ACT	GGC	GGA	GGT	GGC	TCA	GGC	GGA	GGT	GGA		1008
Met	Ser	Glu	Leu	Thr	Glu	Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly		
				325				330						335			
TCT	GGA	GGT	GGA	GGC	TCA	CGG	CTT	GAA	CAG	CCC	AAT	GTC	GCC	ATC	TCC		1056
Ser	Gly	Gly	Gly	Gly	Ser	Arg	Leu	Glu	Gln	Pro	Asn	Val	Ala	Ile	Ser		
			340					345					350				
CTG	TCC	AGG	ACA	GAG	GCC	CTC	AAC	CAC	CAC	AAC	ACT	CTG	GTC	TGT	TCG		1104
Leu	Ser	Arg	Thr	Glu	Ala	Leu	Asn	His	His	Asn	Thr	Leu	Val	Cys	Ser		
		355					360					365					
GTG	ACA	GAT	TTC	TAC	CCA	GCC	AAG	ATC	AAA	GTG	CGC	TGG	TTC	AGG	AAT		1152
Val	Thr	Asp	Phe	Tyr	Pro	Ala	Lys	Ile	Lys	Val	Arg	Trp	Phe	Arg	Asn		
	370					375					380						
GGC	CAG	GAG	GAG	ACA	GTG	GGG	GTC	TCA	TCC	ACA	CAG	CTT	ATT	AGG	AAT		1200
Gly	Gln	Glu	Glu	Thr	Val	Gly	Val	Ser	Ser	Thr	Gln	Leu	Ile	Arg	Asn		
385					390					395					400		
GGG	GAC	TGG	ACC	TTC	CAG	GTC	CTG	GTC	ATG	CTG	GAG	ATG	ACC	CCT	CAT		1248
Gly	Asp	Trp	Thr	Phe	Gln	Val	Leu	Val	Met	Leu	Glu	Met	Thr	Pro	His		
			405					410						415			
CAG	GGA	GAG	GTC	TAC	ACC	TGC	CAT	GTG	GAG	CAT	CCC	AGC	CTG	AAG	AGC		1296
Gln	Gly	Glu	Val	Tyr	Thr	Cys	His	Val	Glu	His	Pro	Ser	Leu	Lys	Ser		
			420					425					430				

CCC ATC ACT GTG GAG TGG AGG GCA CAG TCC GAG TCT GCC CGG AGC AAG  
 Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser Ala Arg Ser Lys  
           435                          440                          445

1341

## (2) INFORMATION FOR SEQ ID NO:57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..588

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT	48
Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val	
1                          5                          10                          15	
TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT	96
Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly	
20                          25                          30	
GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG	144
Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg	
35                          40                          45	
CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG	192
Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu	
50                          55                          60	
CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG	240
Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg	
65                          70                          75                          80	



TCA AAT TTC ACC CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC	288
Ser Asn Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe	
85 90 95	
CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT	336
Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe	
100 105 110	
GTG GAC AAC ATC TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT	384
Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn	
115 120 125	
AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC	432
Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn	
130 135 140	
CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT	480
Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser	
145 150 155 160	
GAT GAT GAC ATT TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG	528
Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu	
165 170 175	
CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG	576
Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu	
180 185 190	
CTG ACA GAG ACT	588
Leu Thr Glu Thr	
195	

## (2) INFORMATION FOR SEQ ID NO:58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 312 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..312

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC AGG ACA GAG GCC	48
Arg Leu Glu Gln Pro Asn Val Ala Ile Ser Leu Ser Arg Thr Glu Ala	
1 5 10 15	
CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA GAT TTC TAC CCA	96
Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro	
20 25 30	
GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG GAG GAG ACA GTG	144
Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val	
35 40 45	
GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC TGG ACC TTC CAG	192
Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln	
50 55 60	
GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA GAG GTC TAC ACC	240
Val Leu Val Met Leu Glu Met Thr Pro His Gln Gly Glu Val Tyr Thr	
65 70 75 80	
TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC ACT GTG GAG TGG	288
Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp	
85 90 95	
AGG GCA CAG TCC GAG TCT GCC CGG	312
Arg Ala Gln Ser Glu Ser Ala Arg	
100 105	

## (2) INFORMATION FOR SEQ ID NO:59:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ser	Arg	Leu	Ser	Lys	Val	Ala	Pro	Val	Ile	Lys	Ala	Arg	Met	Met	Glu
1				5					10					15	
Tyr	Gly	Thr	Thr												
				20											

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Arg	Leu	Ser	Lys	Val	Ala	Pro	Val	Ile	Lys	Ala	Arg	Met	Met	Glu	Tyr
1				5					10					15	

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Lys	Pro	Lys	Ala	Thr	Ala	Glu	Gln	Leu	Lys	Thr	Val	Met	Asp	Asp
1				5					10					15

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Kindsvogel, Wayne  
Gross, Jane A.  
Sheppard, Paul
- (ii) TITLE OF INVENTION: Immune Mediators and Related Methods
- (iii) NUMBER OF SEQUENCES: 121
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Townsend and Townsend and Crew LLP  
(B) STREET: Two Embarcadero Center, Eighth Floor  
(C) CITY: San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
(F) ZIP: 94111-3834
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: US 09/261,811  
(B) FILING DATE: 03-MAR-1999  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/480,002  
(B) FILING DATE: 07-JUN-1995
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/482,133  
(B) FILING DATE: 07-JUN-1995
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/483,241  
(B) FILING DATE: 07-JUN-1995
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 60/005,964  
(B) FILING DATE: 27-OCT-1995
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: US 08/657,581  
(B) FILING DATE: 07-JUN-1996
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Parent, Annette S.  
(B) REGISTRATION NUMBER: 42,058  
(C) REFERENCE/DOCKET NUMBER: 014058-005630US
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (415) 576-0200  
(B) TELEFAX: (415) 576-0300

## (ii) MOLECULE TYPE: DNA

GCGCAAGCTT GAATTCGAGC TCATGGTGTG TCT

33

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 58 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

AATTCGATAT CATGGTGTGT CTGAAGCTCC CTGGAGGCTC CTGCATGACA GCGCTGAC

58

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 58 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

CACTGTCAGC GCTGTCATGC AGGAGCCTCC AGGGAGCTTC AGACACACCA TGATATCG

58

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 60 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACTTCTTTAA AAACATCGTG ACTCCGCGTA CACCCCCGCC ATCGGGAGGC GGGTCAGGTG 60

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 60 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCCACCTG ACCCGCTCC CGATGGCGGG GGTGTACGCG GAGTCACGAT GTTTTAAAG 60

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 59 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGTGACACTG ATGGTGCTGA GCTCCCCACT GGCTTTGTCT GACGAAAACC CAGTAGTGC 59

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 59 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AAGTGCACTA CTGGGTTTTC GTCAGACAAA GCCAGTGGGG AGCTCAGCAC CATCAGTGT 59

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 27 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCCGGCTGAT GCTCCCCGCT GCACTGT

27

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 25 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GCGCTCTAGA TCATATAGTT GGAGC

25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CCAGGGTCTA GATCATAAAG GCCCTGGGTG TCTGGAG

37

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGAGGAATTC GCAGAGACCT CCCAGAGACC AGGATCC

37

CCAGGGTCTA GATCATAAAG GCCCTGGGTG TCTGGAG

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

AACACTCTAG ATCACTGCAG GAGCCCTGCT GGAGGAG

37

## (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 37 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGAGGAATTC TGAGTCCTGG TGACTGCCAT TACCTGT

37

## (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGAGCATCAG CCGGCATCAA AGAAGAACAT

30

## (2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 111 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA



(2) INFORMATION FOR SEQ ID NO:16:

(ii) MOLECULE TYPE: DNA

GGAGGCTCAG GAGGAGGTGG GTCCGGAGAC TCCGAAAGG 39

(2) INFORMATION FOR SEQ ID NO:17:

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CGCGGGATCC GATCGTGGAG GATGATTAA TG 32

(2) INFORMATION FOR SEQ ID NO:18:

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GCCACCTGAT CCACCCCGCA GGGAGGTGGG 30

## (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGTGGATCAG GTGGCGAAGA CGACATTGAG

30

## (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCGGAATTCT TAACTAGTAG CTGGGGTGAA

30

## (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CCGGAATTCT TAACTAGTAG CTGGGGTGGA

30

## (2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 30 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

30

(ii) MOLECULE TYPE: DNA

60

107

(ii) MOLECULE TYPE: DNA

30

(ii) MOLECULE TYPE: DNA

60

72

## (ii) MOLECULE TYPE: DNA

GGCGGAGGTG GCTCAGGCGG AGGTGGATCT GGAGGTGGAG GCTCACGGCT TGAACAGCCC 60  
AAT 63

## (ii) MOLECULE TYPE: DNA

TGAGCCTCCA CCTCCAGATC CACCTCCGCC TGAGCCACCT CCGCCAGTCT CTGTCAGCTC 60  
 TGA 63

(ii) MOLECULE TYPE: DNA

CCGGAATTCT TAACTAGTCT CTGTCAGCTC TGA 33

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Gly Ala Ser Ala Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Gly Gly Ser Gly Gly  
1 -5

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Gly Gly Gly Ser Gly Gly Ser  
1 5

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly  
1 5 10 15

Gly Gly Gly Ser Gly Gly Gly Gly Ser  
20 25

## (2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Asp Glu Asn Pro Val Val His Phe Phe Lys Asn Ile Val Thr Pro Arg  
 1                      5                      10                      15

Thr Pro Pro Pro Ser  
                     20

## (2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 8 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gly Gly Ser Gly Gly Gly Gly Ser  
 1                      5

## (2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGAGGCTCAG GAGGA

15

## (2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro  
1 5 10

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly  
1 5 10

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala Met  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala Met Met Ile Ala Arg Phe  
 1                      5                      10                      15  
 Lys Asn Phe Pro  
                     20

## (2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Pro Gly Gly Ala Ile Ser Asn Met Tyr Ala  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 4 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Glu Arg Leu Glu  
 1

## (2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 5 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear



(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Asp Pro Val Val His  
1 5

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Ser  
1 5 10

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Gly Gly Gly Ser Gly  
1 5

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Gly Gly Gly Ser Gly Gly Ser Gly  
1 5

2004-03-04 10:00:00

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 20 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:47:

(2) INFORMATION FOR SEQ ID NO:48:

(ii) MOLECULE TYPE: DNA

CATCGTGGAG GATGAT

16

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 15 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GAGGATGATT AAATG

15

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 20
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```

Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu
1           5           10           15

Tyr Gly Thr Xaa
                20

```

## (2) INFORMATION FOR SEQ ID NO:51:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 19
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```

Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr
1           5           10           15

Gly Thr Xaa

```

## (2) INFORMATION FOR SEQ ID NO:52:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

Thr Xaa

Xaa

Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Xaa  
1 5 10 15

## (2) INFORMATION FOR SEQ ID NO:55:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Val	Ala	Pro	Val	Ile	Lys	Ala	Arg	Met	Met	Glu	Tyr	Gly	Thr	Xaa
1				5					10					15

## (2) INFORMATION FOR SEQ ID NO:56:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 14
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala	Pro	Val	Ile	Lys	Ala	Arg	Met	Met	Glu	Tyr	Gly	Thr	Xaa
1				5					10				

## (2) INFORMATION FOR SEQ ID NO:57:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

20250318 15:30:00

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Xaa  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:58:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 12
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Xaa  
 1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:59:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Xaa  
 1                      5                      10

"Xaa = threoninamide"

## (2) INFORMATION FOR SEQ ID NO:60:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Lys Ala Arg Met-Met Glu Tyr Gly Thr Xaa  
1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:61:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 18
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = threoninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ser Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr  
1                      5                      10                      15  
Gly Xaa

## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glycine"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Ser Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr  
 1                      5                      10                      15

Xaa

## (2) INFORMATION FOR SEQ ID NO:63:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = tyrosine"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Ser Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Xaa  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:64:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glutamic acid amide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Ser Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Xaa  
 1                      5                      10                      15

"Xaa = tyrosine"



## (2) INFORMATION FOR SEQ ID NO:65:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 14
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = methioninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

Ser	Leu	Ser	Lys_Val	Ala	Pro	Val	Ile	Lys	Ala	Arg	Met	Xaa
1			5					10				

## (2) INFORMATION FOR SEQ ID NO:66:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = methioninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

Ser	Leu	Ser	Lys	Val	Ala	Pro	Val	Ile	Lys	Ala	Arg	Xaa
1				5					10			

## (2) INFORMATION FOR SEQ ID NO:67:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

2025-10-10 10:10:10

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 12  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = argininamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

Ser	Leu	Ser	Lys	Val	Ala	Pro	Val	Ile	Lys	Ala	Xaa
1				5					10		

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 11 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 11  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = alaninamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Ser	Leu	Ser	Lys	Val	Ala	Pro	Val	Ile	Lys	Xaa
1				5					10	

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:  
 (A) NAME/KEY: Modified-site  
 (B) LOCATION: 10  
 (D) OTHER INFORMATION: /product= "OTHER"  
 /note= "Xaa = lysinamide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

Ser	Leu	Ser	Lys	Val	Ala	Pro	Val	Ile	Xaa
1				5					10

20250422 16:33:33

## (2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = isoleucinamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Ser Leu Ser Lys Val Ala Pro Val Xaa  
1 5

## (2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 13 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 13
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glutamic acid amide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Xaa  
1 5 10

## (2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 12 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS:
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
11  
12  
13  
14  
15  
16  
17  
18  
19  
20  
21  
22  
23  
24  
25  
26  
27  
28  
29  
30  
31  
32  
33  
34  
35  
36  
37  
38  
39  
40  
41  
42  
43  
44  
45  
46  
47  
48  
49  
50  
51  
52  
53  
54  
55  
56  
57  
58  
59  
60  
61  
62  
63  
64  
65  
66  
67  
68  
69  
70  
71  
72  
73  
74  
75  
76  
77  
78  
79  
80  
81  
82  
83  
84  
85  
86  
87  
88  
89  
90  
91  
92  
93  
94  
95  
96  
97  
98  
99  
100  
101  
102  
103  
104  
105  
106  
107  
108  
109  
110  
111  
112  
113  
114  
115  
116  
117  
118  
119  
120  
121  
122  
123  
124  
125  
126  
127  
128  
129  
130  
131  
132  
133  
134  
135  
136  
137  
138  
139  
140  
141  
142  
143  
144  
145  
146  
147  
148  
149  
150  
151  
152  
153  
154  
155  
156  
157  
158  
159  
160  
161  
162  
163  
164  
165  
166  
167  
168  
169  
170  
171  
172  
173  
174  
175  
176  
177  
178  
179  
180  
181  
182  
183  
184  
185  
186  
187  
188  
189  
190  
191  
192  
193  
194  
195  
196  
197  
198  
199  
200  
201  
202  
203  
204  
205  
206  
207  
208  
209  
210  
211  
212  
213  
214  
215  
216  
217  
218  
219  
220  
221  
222  
223  
224  
225  
226  
227  
228  
229  
230  
231  
232  
233  
234  
235  
236  
237  
238  
239  
240  
241  
242  
243  
244  
245  
246  
247  
248  
249  
250  
251  
252  
253  
254  
255  
256  
257  
258  
259  
260  
261  
262  
263  
264  
265  
266  
267  
268  
269  
270  
271  
272  
273  
274  
275  
276  
277  
278  
279  
280  
281  
282  
283  
284  
285  
286  
287  
288  
289  
290  
291  
292  
293  
294  
295  
296  
297  
298  
299  
300  
301  
302  
303  
304  
305  
306  
307  
308  
309  
310  
311  
312  
313  
314  
315  
316  
317  
318  
319  
320  
321  
322  
323  
324  
325  
326  
327  
328  
329  
330  
331  
332  
333  
334  
335  
336  
337  
338  
339  
340  
341  
342  
343  
344  
345  
346  
347  
348  
349  
350  
351  
352  
353  
354  
355  
356  
357  
358  
359  
360  
361  
362  
363  
364  
365  
366  
367  
368  
369  
370  
371  
372  
373  
374  
375  
376  
377  
378  
379  
380  
381  
382  
383  
384  
385  
386  
387  
388  
389  
390  
391  
392  
393  
394  
395  
396  
397  
398  
399  
400  
401  
402  
403  
404  
405  
406  
407  
408  
409  
410  
411  
412  
413  
414  
415  
416  
417  
418  
419  
420  
421  
422  
423  
424  
425  
426  
427  
428  
429  
430  
431  
432  
433  
434  
435  
436  
437  
438  
439  
440  
441  
442  
443  
444  
445  
446  
447  
448  
449  
450  
451  
452  
453  
454  
455  
456  
457  
458  
459  
460  
461  
462  
463  
464  
465  
466  
467  
468  
469  
470  
471  
472  
473  
474  
475  
476  
477  
478  
479  
480  
481  
482  
483  
484  
485  
486  
487  
488  
489  
490  
491  
492  
493  
494  
495  
496  
497  
498  
499  
500  
501  
502  
503  
504  
505  
506  
507  
508  
509  
510  
511  
512  
513  
514  
515  
516  
517  
518  
519  
520  
521  
522  
523  
524  
525  
526  
527  
528  
529  
530  
531  
532  
533  
534  
535  
536  
537  
538  
539  
540  
541  
542  
543  
544  
545  
546  
547  
548  
549  
550  
551  
552  
553  
554  
555  
556  
557  
558  
559  
560  
561  
562  
563  
564  
565  
566  
567  
568  
569  
570  
571  
572  
573  
574  
575  
576  
577  
578  
579  
580  
581  
582  
583  
584  
585  
586  
587  
588  
589  
590  
591  
592  
593  
594  
595  
596  
597  
598  
599  
600  
601  
602  
603  
604  
605  
606  
607  
608  
609  
610  
611  
612  
613  
614  
615  
616  
617  
618  
619  
620  
621  
622  
623  
624  
625  
626  
627  
628  
629  
630  
631  
632  
633  
634  
635  
636  
637  
638  
639  
640  
641  
642  
643  
644  
645  
646  
647  
648  
649  
650  
651  
652  
653  
654  
655  
656  
657  
658  
659  
660  
661  
662  
663  
664  
665  
666  
667  
668  
669  
670  
671  
672  
673  
674  
675  
676  
677  
678  
679  
680  
681  
682  
683  
684  
685  
686  
687  
688  
689  
690  
691  
692  
693  
694  
695  
696  
697  
698  
699  
700  
701  
702  
703  
704  
705  
706  
707  
708  
709  
710  
711  
712  
713  
714  
715  
716  
717  
718  
719  
720  
721  
722  
723  
724  
725  
726  
727  
728  
729  
730  
731  
732  
733  
734  
735  
736  
737  
738  
739  
740  
741  
742  
743  
744  
745  
746  
747  
748  
749  
750  
751  
752  
753  
754  
755  
756  
757  
758  
759  
760  
761  
762  
763  
764  
765  
766  
767  
768  
769  
770  
771  
772  
773  
774  
775  
776  
777  
778  
779  
780  
781  
782  
783  
784  
785  
786  
787  
788  
789  
790  
791  
792  
793  
794  
795  
796  
797  
798  
799  
800  
801  
802  
803  
804  
805  
806  
807  
808  
809  
810  
811  
812  
813  
814  
815  
816  
817  
818  
819  
820  
821  
822  
823  
824  
825  
826  
827  
828  
829  
830  
831  
832  
833  
834  
835  
836  
837  
838  
839  
840  
841  
842  
843  
844  
845  
846  
847  
848  
849  
850  
851  
852  
853  
854  
855  
856  
857  
858  
859  
860  
861  
862  
863  
864  
865  
866  
867  
868  
869  
870  
871  
872  
873  
874  
875  
876  
877  
878  
879  
880  
881  
882  
883  
884  
885  
886  
887  
888  
889  
890  
891  
892  
893  
894  
895  
896  
897  
898  
899  
900  
901  
902  
903  
904  
905  
906  
907  
908  
909  
910  
911  
912  
913  
914  
915  
916  
917  
918  
919  
920  
921  
922  
923  
924  
925  
926  
927  
928  
929  
930  
931  
932  
933  
934  
935  
936  
937  
938  
939  
940  
941  
942  
943  
944  
945  
946  
947  
948  
949  
950  
951  
952  
953  
954  
955  
956  
957  
958  
959  
960  
961  
962  
963  
964  
965  
966  
967  
968  
969  
970  
971  
972  
973  
974  
975  
976  
977  
978  
979  
980  
981  
982  
983  
984  
985  
986  
987  
988  
989  
990  
991  
992  
993  
994  
995  
996  
997  
998  
999  
1000

(A) NAME/KEY: Modified-site  
(B) LOCATION: 12  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glutamic acid amide"

Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Xaa  
1                      5                      10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 11  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glutamic acid amide"

Val Ala Pro Val Ile Lys Ala Arg Met Met Xaa  
1 5 10

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 10 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS:  
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 10  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glutamic acid amide"

Ala Pro Val Ile Lys Ala Arg Met Met Xaa  
1 5 10

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 9  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glutamic acid amide"

Pro Val Ile Lys-Ala Arg Met Met Xaa  
1 5

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 12 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS:  
(D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 12  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = methioninamide"

Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Xaa  
1 5 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 11
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = methioninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Ser Lys Val Ala Pro Val Ile Lys Ala Arg Xaa  
1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:78:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 10
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = argininamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Ser Lys Val Ala Pro Val Ile Lys Ala Xaa  
1                      5                      10

## (2) INFORMATION FOR SEQ ID NO:79:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = alaninamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Ser Lys Val Ala Pro Val Ile Lys Xaa  
1                      5

2025-10-10 10:10:10

## (2) INFORMATION FOR SEQ ID NO:80:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 17
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glycynamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

Arg Leu Ser Lys<sup>-</sup>Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr  
 1                      5                      10                      15

Xaa

## (2) INFORMATION FOR SEQ ID NO:81:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = tyrosinamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Xaa  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:82:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glutamic acid amide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Xaa  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:83:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 16
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glycinamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Xaa  
 1                      5                      10                      15

## (2) INFORMATION FOR SEQ ID NO:84:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = tyrosinamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Xaa  
 1                      5                      10                      15

20250304 13:43:44



## (2) INFORMATION FOR SEQ ID NO:85:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 14
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glutamic acid amide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

Leu	Ser	Lys	Val-Ala	Pro	Val	Ile	Lys	Ala	Arg	Met	Met	Xaa
1			5					10				

## (2) INFORMATION FOR SEQ ID NO:86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: 15
- (D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = glycinamide"

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Ser	Lys	Val	Ala	Pro	Val	Ile	Lys	Ala	Arg	Met	Met	Glu	Tyr	Xaa
1				5					10					15

## (2) INFORMATION FOR SEQ ID NO:87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

"Xaa = glutamic acid amide"

(A) NAME/KEY: Modified-site  
(B) LOCATION: 14  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = tyrosinamide"

Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Xaa  
1 5 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: Modified-site  
(B) LOCATION: 8  
(D) OTHER INFORMATION: /product= "OTHER"  
/note= "Xaa = lysinamide"

Ser Lys Val Ala Pro Val Ile Xaa  
1 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

Lys Pro Lys Ala Thr Ala Glu Gln Leu Lys Thr Val Met Asp Asp  
1 5 10 15

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 243 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

ATC	AAA	GAA	GAA	CAT	GTG	ATC	ATC	CAG	GCC	GAG	TTC	TAT	CTG	AAT	CCT	48
Ile	Lys	Glu	Glu	His	Val	Ile	Ile	Gln	Ala	Glu	Phe	Tyr	Leu	Asn	Pro	
1				5				10					15			
GAC	CAA	TCA	GGC	GAA	TTT	ATG	TTT	GAC	TTT	GAT	GGT	GAT	GAG	ATT	TTC	96
Asp	Gln	Ser	Gly	Glu	Phe	Met	Phe	Asp	Phe	Asp	Gly	Asp	Glu	Ile	Phe	
			20					25					30			
CAT	GTG	GAT	ATG	GCA	AAG	AAG	GAG	ACG	GTC	TGG	CGG	CTT	GAA	GAA	TTT	144
His	Val	Asp	Met	Ala	Lys	Lys	Glu	Thr	Val	Trp	Arg	Leu	Glu	Glu	Phe	
			35				40					45				
GGA	CGA	TTT	GCC	AGC	TTT	GAG	GCT	CAA	GGT	GCA	TTG	GCC	AAC	ATA	GCT	192
Gly	Arg	Phe	Ala	Ser	Phe	Glu	Ala	Gln	Gly	Ala	Leu	Ala	Asn	Ile	Ala	
			50			55					60					
GTG	GAC	AAA	GCC	AAC	CTG	GAA	ATC	ATG	ACA	AAG	CGC	TCC	AAC	TAT	ATG	240
Val	Asp	Lys	Ala	Asn	Leu	Glu	Ile	Met	Thr	Lys	Arg	Ser	Asn	Tyr	Met	
65					70					75					80	
ATC																243
Ile																

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

Ile	Lys	Glu	Glu	His	Val	Ile	Ile	Gln	Ala	Glu	Phe	Tyr	Leu	Asn	Pro	
1				5				10					15			
Asp	Gln	Ser	Gly	Glu	Phe	Met	Phe	Asp	Phe	Asp	Gly	Asp	Glu	Ile	Phe	
			20					25					30			
His	Val	Asp	Met	Ala	Lys	Lys	Glu	Thr	Val	Trp	Arg	Leu	Glu	Glu	Phe	
			35				40					45				
Gly	Arg	Phe	Ala	Ser	Phe	Glu	Ala	Gln	Gly	Ala	Leu	Ala	Asn	Ile	Ala	
			50			55					60					

Val Asp Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Met  
 65 70 75 80

Ile

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

GAC	GAA	AAC	CCA	GTA	GTG	CAC	TTC	TTT	AAA	AAC	ATC	GTG	ACT	CCG	CGT	48
Asp	Glu	Asn	Pro	Val	Val	His	Phe	Phe	Lys	Asn	Ile	Val	Thr	Pro	Arg	
1				5					10					15		
ACA	CCC	CCG	CCA	TCG	GGA	GGC	GGG	TCA	GGT	GGA	TCC	GGG	GAC	ACC	CGA	96
Thr	Pro	Pro	Pro	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Asp	Thr	Arg	
			20					25					30			
CCA	CGT	TTC	CTG	TGG	CAG	CCT	AAG	AGG	GAG	TGT	CAT	TTC	TTC	AAT	GGG	144
Pro	Arg	Phe	Leu	Trp	Gln	Pro	Lys	Arg	Glu	Cys	His	Phe	Phe	Asn	Gly	
		35					40					45				
ACG	GAG	CGG	GTG	CGG	TTC	CTG	GAC	AGA	TAC	TTC	TAT	AAC	CAG	GAG	GAG	192
Thr	Glu	Arg	Val	Arg	Phe	Leu	Asp	Arg	Tyr	Phe	Tyr	Asn	Gln	Glu	Glu	
	50					55				60						
TCC	GTG	CGT	TTC	GAC	AGC	GAC	GTG	GGG	GAG	TTC	CGG	GCG	GTG	ACG	GAG	240
Ser	Val	Arg	Phe	Asp	Ser	Asp	Val	Gly	Glu	Phe	Arg	Ala	Val	Thr	Glu	
65				70					75					80		
CTG	GGG	CGG	CCT	GAC	GCT	GAG	TAC	TGG	AAC	AGC	CAG	AAG	GAC	ATC	CTG	288
Leu	Gly	Arg	Pro	Asp	Ala	Glu	Tyr	Trp	Asn	Ser	Gln	Lys	Asp	Ile	Leu	
			85					90					95			
GAG	CAG	GCG	CGG	GCC	GCG	GTG	GAC	ACC	TAC	TGC	AGA	CAC	AAC	TAC	GGG	336
Glu	Gln	Ala	Arg	Ala	Ala	Val	Asp	Thr	Tyr	Cys	Arg	His	Asn	Tyr	Gly	
		100					105					110				
GTT	GTG	GAG	AGC	TTC	ACA	GTG	CAG	CGG	GGA	GCA	TCA	GCC	GGC	ATC	AAA	384
Val	Val	Glu	Ser	Phe	Thr	Val	Gln	Arg	Gly	Ala	Ser	Ala	Gly	Ile	Lys	
	115					120					125					
GAA	GAA	CAT	GTG	ATC	ATC	CAG	GCC	GAG	TTC	TAT	CTG	AAT	CCT	GAC	CAA	432
Glu	Glu	His	Val	Ile	Ile	Gln	Ala	Glu	Phe	Tyr	Leu	Asn	Pro	Asp	Gln	
	130					135					140					

20250423 13:43:04

TCA GGC GAA TTT ATG TTT GAC TTT GAT GGT GAT GAG ATT TTC CAT GTG	480
Ser Gly Glu Phe Met Phe Asp Phe Asp Gly Asp Glu Ile Phe His Val	
145 150 155 160	
GAT ATG GCA AAG AAG GAG ACG GTC TGG CGG CTT GAA GAA TTT GGA CGA	528
Asp Met Ala Lys Lys Glu Thr Val Trp Arg Leu Glu Glu Phe Gly Arg	
165 170 175	
TTT GCC AGC TTT GAG GCT CAA GGT GCA TTG GCC AAC ATA GCT GTG GAC	576
Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp	
180 185 190	
AAA GCC AAC CTG GAA ATC ATG ACA AAG CGC TCC AAC TAT ATG ATC	621
Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Met Ile	
195 200 205	

## (2) INFORMATION FOR SEQ ID NO:93:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 207 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

Asp	Glu	Asn	Pro	Val	Val	His	Phe	Phe	Lys	Asn	Ile	Val	Thr	Pro	Arg	1	5	10	15
Thr	Pro	Pro	Pro	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Ser	Gly	Asp	Thr	Arg	20	25	30	
Pro	Arg	Phe	Leu	Trp	Gln	Pro	Lys	Arg	Glu	Cys	His	Phe	Phe	Asn	Gly	35	40	45	
Thr	Glu	Arg	Val	Arg	Phe	Leu	Asp	Arg	Tyr	Phe	Tyr	Asn	Gln	Glu	Glu	50	55	60	
Ser	Val	Arg	Phe	Asp	Ser	Asp	Val	Gly	Glu	Phe	Arg	Ala	Val	Thr	Glu	65	70	75	80
Leu	Gly	Arg	Pro	Asp	Ala	Glu	Tyr	Trp	Asn	Ser	Gln	Lys	Asp	Ile	Leu	85	90	95	
Glu	Gln	Ala	Arg	Ala	Ala	Val	Asp	Thr	Tyr	Cys	Arg	His	Asn	Tyr	Gly	100	105	110	
Val	Val	Glu	Ser	Phe	Thr	Val	Gln	Arg	Gly	Ala	Ser	Ala	Gly	Ile	Lys	115	120	125	
Glu	Glu	His	Val	Ile	Ile	Gln	Ala	Glu	Phe	Tyr	Leu	Asn	Pro	Asp	Gln	130	135	140	
Ser	Gly	Glu	Phe	Met	Phe	Asp	Phe	Asp	Gly	Asp	Glu	Ile	Phe	His	Val	145	150	155	160
Asp	Met	Ala	Lys	Lys	Glu	Thr	Val	Trp	Arg	Leu	Glu	Glu	Phe	Gly	Arg	165	170	175	

Phe Ala Ser Phe Glu Ala Gln Gly Ala Leu Ala Asn Ile Ala Val Asp  
                   180                  185                  190  
 Lys Ala Asn Leu Glu Ile Met Thr Lys Arg Ser Asn Tyr Met Ile  
                   195                  200                  205

## (2) INFORMATION FOR SEQ ID NO:94:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..273

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

GGA GAC TCC GAA AGG CAT TTC GTG CAC CAG TTC AAG GGC GAG TGC TAC	48
Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly Glu Cys Tyr	
1                                  5                                  10                                  15	
TTC ACC AAC GGG ACG CAG CGC ATA CGG CTC GTG ACC AGA TAC ATC TAC	96
Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr	
20                                  25                                  30	
AAC CGG GAG GAG TAC CTG CGC TTC GAC AGC GAC GTG GGC GAG TAC CGC	144
Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg	
35                                  40                                  45	
GCG GTG ACC GAG CTG GGG CGG CAC TCA GCC GAG TAC TAC AAT AAG CAG	192
Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr Asn Lys Gln	
50                                  55                                  60	
TAC CTG GAG CGA ACG CGG GCC GAG CTG GAC ACG GCG TGC AGA CAC AAC	240
Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys Arg His Asn	
65                                  70                                  75                                  80	
TAC GAG GAG ACG GAG GTC CCC ACC TCC CTG CGG	273
Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg	
85                                  90	

## (2) INFORMATION FOR SEQ ID NO:95:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

"GCGGT" TGGTGGT

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly Glu Cys Tyr  
 1 5 10 15  
 Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg Tyr Ile Tyr  
 20 25 30  
 Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg  
 35 40 45  
 Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr Asn Lys Gln  
 50 55 60  
 Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys Arg His Asn  
 65 70 75 80  
 Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg  
 85 90

## (2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 261 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..261

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT 48  
 Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val  
 1 5 10 15  
 TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT 96  
 Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly  
 20 25 30  
 GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG 144  
 Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg  
 35 40 45  
 CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG 192  
 Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu  
 50 55 60  
 CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG 240  
 Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg  
 65 70 75 80

TCA AAT TTC ACC CCA GCT ACT  
 Ser Asn Phe Thr Pro Ala Thr  
 85

261

## (2) INFORMATION FOR SEQ ID NO:97:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val  
 1 5 10 15  
 Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly  
 20 25 30  
 Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg  
 35 40 45  
 Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu  
 50 55 60  
 Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg  
 65 70 75 80  
 Ser Asn Phe Thr Pro Ala Thr  
 85

## (2) INFORMATION FOR SEQ ID NO:98:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 654 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..654

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGT CGC CTC TCG AAG GTG GCT CCA GTG ATT AAA GCC AGA ATG ATG GAG 48  
 Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu  
 1 5 10 15  
 TAT GGA ACC ACA GGA GGT GGA GGC TCT GGA GGT GGA GGC TCA GGA GGA 96  
 Tyr Gly Thr Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly  
 20 25 30



GGT GGG TCC GGA GAC TCC GAA AGG CAT TTC GTG CAC CAG TTC AAG GGC	144
Gly Gly Ser Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly	
35 40 45	
GAG TGC TAC TTC ACC AAC GGG ACG CAG CGC ATA CGG CTC GTG ACC AGA	192
Glu Cys Tyr Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg	
50 55 60	
TAC ATC TAC AAC CGG GAG GAG TAC CTG CGC TTC GAC AGC GAC GTG GGC	240
Tyr Ile Tyr Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly	
65 70 75 80	
GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CAC TCA GCC GAG TAC TAC	288
Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr	
85 90 95	
AAT AAG CAG TAC CTG GAG CGA ACG CGG GCC GAG CTG GAC ACG GCG TGC	336
Asn Lys Gln Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys	
100 105 110	
AGA CAC AAC TAC GAG GAG ACG GAG GTC CCC ACC TCC CTG CGG GGT GGA	384
Arg His Asn Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg Gly Gly	
115 120 125	
TCA GGT GGC GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT	432
Ser Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly	
130 135 140	
ACA ACT GTT TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA	480
Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu	
145 150 155 160	
TTT GAT GGT GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT	528
Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr	
165 170 175	
GTC TGG AGG CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA	576
Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln	
180 185 190	
GGT GGA CTG CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG	624
Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu	
195 200 205	
ACT AAG AGG TCA AAT TTC ACC CCA GCT ACT	654
Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr	
210 215	

## (2) INFORMATION FOR SEQ ID NO:99:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

Ser	Arg	Leu	Ser	Lys	Val	Ala	Pro	Val	Ile	Lys	Ala	Arg	Met	Met	Glu
1				5					10						15
Tyr	Gly	Thr	Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly
			20					25					30		
Gly	Gly	Ser	Gly	Asp	Ser	Glu	Arg	His	Phe	Val	His	Gln	Phe	Lys	Gly
		35					40					45			
Glu	Cys	Tyr	Phe	Thr	Asn	Gly	Thr	Gln	Arg	Ile	Arg	Leu	Val	Thr	Arg
	50					55					60				
Tyr	Ile	Tyr	Asn	Arg	Glu	Glu	Tyr	Leu	Arg	Phe	Asp	Ser	Asp	Val	Gly
65					70					75					80
Glu	Tyr	Arg	Ala	Val	Thr	Glu	Leu	Gly	Arg	His	Ser	Ala	Glu	Tyr	Tyr
				85					90					95	
Asn	Lys	Gln	Tyr	Leu	Glu	Arg	Thr	Arg	Ala	Glu	Leu	Asp	Thr	Ala	Cys
			100					105					110		
Arg	His	Asn	Tyr	Glu	Glu	Thr	Glu	Val	Pro	Thr	Ser	Leu	Arg	Gly	Gly
		115					120					125			
Ser	Gly	Gly	Glu	Asp	Asp	Ile	Glu	Ala	Asp	His	Val	Gly	Phe	Tyr	Gly
	130					135					140				
Thr	Thr	Val	Tyr	Gln	Ser	Pro	Gly	Asp	Ile	Gly	Gln	Tyr	Thr	His	Glu
145					150					155					160
Phe	Asp	Gly	Asp	Glu	Leu	Phe	Tyr	Val	Asp	Leu	Asp	Lys	Lys	Lys	Thr
				165					170					175	
Val	Trp	Arg	Leu	Pro	Glu	Phe	Gly	Gln	Leu	Ile	Leu	Phe	Glu	Pro	Gln
			180					185					190		
Gly	Gly	Leu	Gln	Asn	Ile	Ala	Ala	Glu	Lys	His	Asn	Leu	Gly	Ile	Leu
		195					200					205			
Thr	Lys	Arg	Ser	Asn	Phe	Thr	Pro	Ala	Thr						
210						215									

(1) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 273 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

```
(ix) FEATURE:
      (A) NAME/KEY: CDS
      (B) LOCATION: 1..273
```

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

GGA GAC TCC GAA AGG CAT TTC GTG TTC CAG TTC AAG GGC GAG TGC TAC	48
Gly Asp Ser Glu Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr	
1 5 10 15	
TTC ACC AAC GGG ACG CAG CGC ATA CGA TCT GTG GAC AGA TAC ATC TAC	96
Phe Thr Asn Gly Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr	
20 25 30	
AAC CGG GAG GAG TAC CTG CGC TTC GAC AGC GAC GTG GGC GAG TAC CGC	144
Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg	
35 40 45	
GCG GTG ACC GAG CTG GGG CGG CCA GAC CCC GAG TAC TAC AAT AAG CAG	192
Ala Val Thr Glu Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln	
50 55 60	
TAC CTG GAG CAA ACG CGG GCC GAG CTG GAC ACG GTG TGC AGA CAC AAC	240
Tyr Leu Glu Gln Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn	
65 70 75 80	
TAC GAG GGG GTG GAG ACC CAC ACC TCC CTG CGG	273
Tyr Glu Gly Val Glu Thr His Thr Ser Leu Arg	
85 90	

## (2) INFORMATION FOR SEQ ID NO:101:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

Gly Asp Ser Glu Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr
1 5 10 15
Phe Thr Asn Gly Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr
20 25 30
Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg
35 40 45
Ala Val Thr Glu Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln
50 55 60
Tyr Leu Glu Gln Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn
65 70 75 80
Tyr Glu Gly Val Glu Thr His Thr Ser Leu Arg
85 90

## (2) INFORMATION FOR SEQ ID NO:102:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 261 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (ix) FEATURE:  
 (A) NAME/KEY: CDS  
 (B) LOCATION: 1..261

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA	48
Glu Asp Asp Ile Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val	
1 5 10 15	
TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT	96
Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly	
20 25 30	
GAT GAG TGG TTC TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG	144
Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met	
35 40 45	
CTT CCT GAG TTT GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG	192
Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu	
50 55 60	
CAA AAC ATA GCT ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG	240
Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg	
65 70 75 80	
TCA AAT TCC ACC CCA GCT ACT	261
Ser Asn Ser Thr Pro Ala Thr	
85	

## (2) INFORMATION FOR SEQ ID NO:103:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 87 amino acids  
 (B) TYPE: amino acid  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

Glu Asp Asp Ile Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val	
1 5 10 15	
Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly	
20 25 30	

Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met  
           35                          40                          45

Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu  
           50                          55                          60

Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg  
           65                          70                          75                          80

Ser Asn Ser Thr Pro Ala Thr  
                                   85

## (2) INFORMATION FOR SEQ ID NO:104:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS  
 (B) LOCATION: 1..633

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTC	TTT	AAA	AAC	ATC	GTG	ACT	CCG	CGT	ACA	CCC	CCG	CCA	GGA	GGT	GGA	48
Phe	Phe	Lys	Asn	Ile	Val	Thr	Pro	Arg	Thr	Pro	Pro	Pro	Gly	Gly	Gly	
1				5				10					15			
GGC	TCT	GGA	GGT	GGA	GGC	TCA	GGA	GGA	GGT	GGG	TCC	GGA	GAC	TCC	GAA	96
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Asp	Ser	Glu	
		20						25					30			
AGG	CAT	TTC	GTG	TTC	CAG	TTC	AAG	GGC	GAG	TGC	TAC	TTC	ACC	AAC	GGG	144
Arg	His	Phe	Val	Phe	Gln	Phe	Lys	Gly	Glu	Cys	Tyr	Phe	Thr	Asn	Gly	
		35					40					45				
ACG	CAG	CGC	ATA	CGA	TCT	GTG	GAC	AGA	TAC	ATC	TAC	AAC	CGG	GAG	GAG	192
Thr	Gln	Arg	Ile	Arg	Ser	Val	Asp	Arg	Tyr	Ile	Tyr	Asn	Arg	Glu	Glu	
	50					55					60					
TAC	CTG	CGC	TTC	GAC	AGC	GAC	GTG	GGC	GAG	TAC	CGC	GCG	GTG	ACC	GAG	240
Tyr	Leu	Arg	Phe	Asp	Ser	Asp	Val	Gly	Glu	Tyr	Arg	Ala	Val	Thr	Glu	
65				70				75						80		
CTG	GGG	CGG	CCA	GAC	CCC	GAG	TAC	TAC	AAT	AAG	CAG	TAC	CTG	GAG	CAA	288
Leu	Gly	Arg	Pro	Asp	Pro	Glu	Tyr	Tyr	Asn	Lys	Gln	Tyr	Leu	Glu	Gln	
			85					90					95			
ACG	CGG	GCC	GAG	CTG	GAC	ACG	GTG	TGC	AGA	CAC	AAC	TAC	GAG	GGG	GTG	336
Thr	Arg	Ala	Glu	Leu	Asp	Thr	Val	Cys	Arg	His	Asn	Tyr	Glu	Gly	Val	
		100						105					110			

bioRxiv preprint doi: <https://doi.org/10.1101/000000>; this version posted January 1, 2014. The copyright holder for this preprint (which was not certified by peer review) is the author/funder, who has granted bioRxiv a license to display the preprint in perpetuity. It is made available under aCC-BY-NC-ND 4.0 International license.

GAG ACC CAC ACC TCC CTG CGG GGT GGA TCA GGT GGC GAA GAC GAC ATT	384
Glu Thr His Thr Ser Leu Arg Gly Gly Ser Gly Gly Glu Asp Asp Ile	
115 120 125	
GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA TAT CAG TCT CCT	432
Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro	
130 135 140	
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TGG TTC	480
Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Trp Phe	
145 150 155 160	
TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG CTT CCT GAG TTT	528
Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met Leu Pro Glu Phe	
165 170 175	
GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG CAA AAC ATA GCT	576
Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala	
180 185 190	
ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG TCA AAT TCC ACC	624
Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr	
195 200 205	
CCA GCT ACT	633
Pro Ala Thr	
210	

## (2) INFORMATION FOR SEQ ID NO:105:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly	
1 5 10 15	
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Asp Ser Glu	
20 25 30	
Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly	
35 40 45	
Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr Asn Arg Glu Glu	
50 55 60	
Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu	
65 70 75 80	
Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Gln	
85 90 95	
Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn Tyr Glu Gly Val	
100 105 110	

Glu Thr His Thr Ser Leu Arg Gly Gly Ser Gly Gly Glu Asp Asp Ile  
 115 120 125  
 Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro  
 130 135 140  
 Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Trp Phe  
 145 150 155 160  
 Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met Leu Pro Glu Phe  
 165 170 175  
 Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala  
 180 185 190  
 Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr  
 195 200 205  
 Pro Ala Thr  
 210

## (2) INFORMATION FOR SEQ ID NO:106:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 312 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..312

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC CTG TCC AGG ACA GAG GCC	48
Arg Leu Glu Gln Pro Asn Val Ala Ile Ser Leu Ser Arg Thr Glu Ala	
1 5 10 15	
CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG GTG ACA GAT TTC TAC CCA	96
Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro	
20 25 30	
GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT GGC CAG GAG GAG ACA GTG	144
Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val	
35 40 45	
GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC TGG ACC TTC CAG	192
Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln	
50 55 60	
GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT CAG GGA GAG GTC TAC ACC	240
Val Leu Val Met Leu Glu Met Thr Pro His Gln Gly Glu Val Tyr Thr	
65 70 75 80	

TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC CCC ATC ACT GTG GAG TGG 288  
 Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp  
                     85                    90                    95

AGG GCA CAG TCC GAG TCT GCC CGG 312  
 Arg Ala Gln Ser Glu Ser Ala Arg  
                     100

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Arg Leu Glu Gln Pro Asn Val Ala Ile Ser Leu Ser Arg Thr Glu Ala  
   1                    5                    10                    15  
 Leu Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro  
                     20                    25                    30  
 Ala Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val  
                     35                    40                    45  
 Gly Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln  
                     50                    55                    60  
 Val Leu Val Met Leu Glu Met Thr Pro His Gln Gly Glu Val Tyr Thr  
                     65                    70                    75                    80  
 Cys His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp  
                     85                    90                    95  
 Arg Ala Gln Ser Glu Ser Ala Arg  
                     100

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 588 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..588

2025 RELEASE UNDER E.O. 14176



## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT ACA ACT GTT	48
Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val	
1 5 10 15	
TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT	96
Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly	
20 25 30	
GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT GTC TGG AGG	144
Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg	
35 40 45	
CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA GGT GGA CTG	192
Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu	
50 55 60	
CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG ACT AAG AGG	240
Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg	
65 70 75 80	
TCA AAT TTC ACC CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC	288
Ser Asn Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe	
85 90 95	
CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT	336
Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe	
100 105 110	
GTG GAC AAC ATC TTC CCA CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT	384
Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn	
115 120 125	
AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG ACC AGC TTC CTC GTC AAC	432
Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn	
130 135 140	
CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT	480
Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser	
145 150 155 160	
GAT GAT GAC ATT TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG	528
Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu	
165 170 175	
CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG	576
Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu	
180 185 190	
CTG ACA GAG ACT	588
Leu Thr Glu Thr	
195	

## (2) INFORMATION FOR SEQ ID NO:109:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly Thr Thr Val  
1 5 10 15  
Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly  
20 25 30  
Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr Val Trp Arg  
35 40 45  
Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln Gly Gly Leu  
50 55 60  
Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu Thr Lys Arg  
65 70 75 80  
Ser Asn Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe  
85 90 95  
Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe  
100 105 110  
Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn  
115 120 125  
Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn  
130 135 140  
Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser  
145 150 155 160  
Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu  
165 170 175  
Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu  
180 185 190  
Leu Thr Glu Thr  
195

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1344 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1344

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AGT CGC CTC TCG AAG GTG GCT CCA GTG ATT AAA GCC AGA ATG ATG GAG	48
Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu	
1 5 10 15	
TAT GGA ACC ACA GGA GGT GGA GGC TCT GGA GGT GGA GGC TCA GGA GGA	96
Tyr Gly Thr Thr Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly	
20 25 30	
GGT GGG TCC GGA GAC TCC GAA AGG CAT TTC GTG CAC CAG TTC AAG GGC	144
Gly Gly Ser Gly Asp Ser Glu Arg His Phe Val His Gln Phe Lys Gly	
35 40 45	
GAG TGC TAC TTC ACC AAC GGG ACG CAG CGC ATA CGG CTC GTG ACC AGA	192
Glu Cys Tyr Phe Thr Asn Gly Thr Gln Arg Ile Arg Leu Val Thr Arg	
50 55 60	
TAC ATC TAC AAC CGG GAG GAG TAC CTG CGC TTC GAC AGC GAC GTG GGC	240
Tyr Ile Tyr Asn Arg Glu Glu Tyr Leu Arg Phe Asp Ser Asp Val Gly	
65 70 75 80	
GAG TAC CGC GCG GTG ACC GAG CTG GGG CGG CAC TCA GCC GAG TAC TAC	288
Glu Tyr Arg Ala Val Thr Glu Leu Gly Arg His Ser Ala Glu Tyr Tyr	
85 90 95	
AAT AAG CAG TAC CTG GAG CGA ACG CGG GCC GAG CTG GAC ACG GCG TGC	336
Asn Lys Gln Tyr Leu Glu Arg Thr Arg Ala Glu Leu Asp Thr Ala Cys	
100 105 110	
AGA CAC AAC TAC GAG GAG ACG GAG GTC CCC ACC TCC CTG CGG GGT GGA	384
Arg His Asn Tyr Glu Glu Thr Glu Val Pro Thr Ser Leu Arg Gly Gly	
115 120 125	
TCA GGT GGC GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC TTC TAT GGT	432
Ser Gly Gly Glu Asp Asp Ile Glu Ala Asp His Val Gly Phe Tyr Gly	
130 135 140	
ACA ACT GTT TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA	480
Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu	
145 150 155 160	
TTT GAT GGT GAT GAG TTG TTC TAT GTG GAC TTG GAT AAG AAG AAA ACT	528
Phe Asp Gly Asp Glu Leu Phe Tyr Val Asp Leu Asp Lys Lys Lys Thr	
165 170 175	
GTC TGG AGG CTT CCT GAG TTT GGC CAA TTG ATA CTC TTT GAG CCC CAA	576
Val Trp Arg Leu Pro Glu Phe Gly Gln Leu Ile Leu Phe Glu Pro Gln	
180 185 190	
GGT GGA CTG CAA AAC ATA GCT GCA GAA AAA CAC AAC TTG GGA ATC TTG	624
Gly Gly Leu Gln Asn Ile Ala Ala Glu Lys His Asn Leu Gly Ile Leu	
195 200 205	
ACT AAG AGG TCA AAT TTC ACC CCA GCT ACC AAT GAG GCT CCT CAA GCG	672
Thr Lys Arg Ser Asn Phe Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala	
210 215 220	
ACT GTG TTC CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC AAC ACC CTT	720
Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu	
225 230 235 240	

ATC TGC TTT GTG GAC AAC ATC TTC CCA CCT GTG ATC AAC ATC ACA TGG	768
Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp	
245 250 255	
CTC AGA AAT AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG ACC AGC TTC	816
Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe	
260 265 270	
CTC GTC AAC CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT CTC ACC TTC	864
Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe	
275 280 285	
ATC CCT TCT GAT GAT GAC ATT TAT GAC TGC AAG GTG GAG CAC TGG GGC	912
Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly	
290 295 300	
CTG GAG GAG CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT CCA GCC CCC	960
Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro	
305 310 315 320	
ATG TCA GAG CTG ACA GAG ACT GGC GGA GGT GGC TCA GGC GGA GGT GGA	1008
Met Ser Glu Leu Thr Glu Thr Gly Gly Gly Ser Gly Gly Gly Gly	
325 330 335	
TCT GGA GGT GGA GGC TCA CGG CTT GAA CAG CCC AAT GTC GCC ATC TCC	1056
Ser Gly Gly Gly Ser Arg Leu Glu Gln Pro Asn Val Ala Ile Ser	
340 345 350	
CTG TCC AGG ACA GAG GCC CTC AAC CAC CAC AAC ACT CTG GTC TGT TCG	1104
Leu Ser Arg Thr Glu Ala Leu Asn His His Asn Thr Leu Val Cys Ser	
355 360 365	
GTG ACA GAT TTC TAC CCA GCC AAG ATC AAA GTG CGC TGG TTC AGG AAT	1152
Val Thr Asp Phe Tyr Pro Ala Lys Ile Lys Val Arg Trp Phe Arg Asn	
370 375 380	
GGC CAG GAG GAG ACA GTG GGG GTC TCA TCC ACA CAG CTT ATT AGG AAT	1200
Gly Gln Glu Glu Thr Val Gly Val Ser Ser Thr Gln Leu Ile Arg Asn	
385 390 395 400	
GGG GAC TGG ACC TTC CAG GTC CTG GTC ATG CTG GAG ATG ACC CCT CAT	1248
Gly Asp Trp Thr Phe Gln Val Leu Val Met Leu Glu Met Thr Pro His	
405 410 415	
CAG GGA GAG GTC TAC ACC TGC CAT GTG GAG CAT CCC AGC CTG AAG AGC	1296
Gln Gly Glu Val Tyr Thr Cys His Val Glu His Pro Ser Leu Lys Ser	
420 425 430	
CCC ATC ACT GTG GAG TGG AGG GCA CAG TCC GAG TCT GCC CGG AGC AAG	1344
Pro Ile Thr Val Glu Trp Arg Ala Gln Ser Glu Ser Ala Arg Ser Lys	
435 440 445	

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 448 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Ser	Arg	Leu	Ser	Lys	Val	Ala	Pro	Val	Ile	Lys	Ala	Arg	Met	Met	Glu	1	5	10	15
Tyr	Gly	Thr	Thr	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	20	25	30	
Gly	Gly	Ser	Gly	Asp	Ser	Glu	Arg	His	Phe	Val	His	Gln	Phe	Lys	Gly	35	40	45	
Glu	Cys	Tyr	Phe	Thr	Asn	Gly	Thr	Gln	Arg	Ile	Arg	Leu	Val	Thr	Arg	50	55	60	
Tyr	Ile	Tyr	Asn	Arg	Glu	Glu	Tyr	Leu	Arg	Phe	Asp	Ser	Asp	Val	Gly	65	70	75	80
Glu	Tyr	Arg	Ala	Val	Thr	Glu	Leu	Gly	Arg	His	Ser	Ala	Glu	Tyr	Tyr	85	90	95	
Asn	Lys	Gln	Tyr	Leu	Glu	Arg	Thr	Arg	Ala	Glu	Leu	Asp	Thr	Ala	Cys	100	105	110	
Arg	His	Asn	Tyr	Glu	Glu	Thr	Glu	Val	Pro	Thr	Ser	Leu	Arg	Gly	Gly	115	120	125	
Ser	Gly	Gly	Glu	Asp	Asp	Ile	Glu	Ala	Asp	His	Val	Gly	Phe	Tyr	Gly	130	135	140	
Thr	Thr	Val	Tyr	Gln	Ser	Pro	Gly	Asp	Ile	Gly	Gln	Tyr	Thr	His	Glu	145	150	155	160
Phe	Asp	Gly	Asp	Glu	Leu	Phe	Tyr	Val	Asp	Leu	Asp	Lys	Lys	Lys	Thr	165	170	175	
Val	Trp	Arg	Leu	Pro	Glu	Phe	Gly	Gln	Leu	Ile	Leu	Phe	Glu	Pro	Gln	180	185	190	
Gly	Gly	Leu	Gln	Asn	Ile	Ala	Ala	Glu	Lys	His	Asn	Leu	Gly	Ile	Leu	195	200	205	
Thr	Lys	Arg	Ser	Asn	Phe	Thr	Pro	Ala	Thr	Asn	Glu	Ala	Pro	Gln	Ala	210	215	220	
Thr	Val	Phe	Pro	Lys	Ser	Pro	Val	Leu	Leu	Gly	Gln	Pro	Asn	Thr	Leu	225	230	235	240
Ile	Cys	Phe	Val	Asp	Asn	Ile	Phe	Pro	Pro	Val	Ile	Asn	Ile	Thr	Trp	245	250	255	
Leu	Arg	Asn	Ser	Lys	Ser	Val	Thr	Asp	Gly	Val	Tyr	Glu	Thr	Ser	Phe	260	265	270	
Leu	Val	Asn	Arg	Asp	His	Ser	Phe	His	Lys	Leu	Ser	Tyr	Leu	Thr	Phe	275	280	285	
Ile	Pro	Ser	Asp	Asp	Asp	Ile	Tyr	Asp	Cys	Lys	Val	Glu	His	Trp	Gly	290	295	300	
Leu	Glu	Glu	Pro	Val	Leu	Lys	His	Trp	Glu	Pro	Glu	Ile	Pro	Ala	Pro	305	310	315	320

CGG	CTT	GAA	CAG	CCC	AAT	GTC	GTC	ATC	TCC	CTG	TCC	AGG	ACA	GAG	GCC	48
Arg	Leu	Glu	Gln	Pro	Asn	Val	Val	Ile	Ser	Leu	Ser	Arg	Thr	Glu	Ala	
1				5					10					15		
CTC	AAC	CAC	CAC	AAC	ACT	CTG	GTC	TGC	TCA	GTG	ACA	GAT	TTC	TAC	CCA	96
Leu	Asn	His	His	Asn	Thr	Leu	Val	Cys	Ser	Val	Thr	Asp	Phe	Tyr	Pro	
			20					25					30			
GCC	AAG	ATC	AAA	GTG	CGC	TGG	TTC	CGG	AAT	GGC	CAG	GAG	GAG	ACG	GTG	144
Ala	Lys	Ile	Lys	Val	Arg	Trp	Phe	Arg	Asn	Gly	Gln	Glu	Glu	Thr	Val	
		35				40						45				
GGG	GTC	TCA	TCC	ACA	CAG	CTT	ATT	AGG	AAT	GGG	GAC	TGG	ACC	TTC	CAG	192
Gly	Val	Ser	Ser	Thr	Gln	Leu	Ile	Arg	Asn	Gly	Asp	Trp	Thr	Phe	Gln	
	50					55					60					

GTC	CTG	GTC	ATG	CTG	GAG	ATG	ACC	CCT	CGG	CGG	GGA	GAG	GTC	TAC	ACC	240
Val	Leu	Val	Met	Leu	Glu	Met	Thr	Pro	Arg	Arg	Gly	Glu	Val	Tyr	Thr	
65					70					75					80	
TGC	CAC	GTG	GAG	CAT	CCG	AGC	CTG	AAG	AGC	CCC	ATC	ACT	GTG	GAG	TGG	288
Cys	His	Val	Glu	His	Pro	Ser	Leu	Lys	Ser	Pro	Ile	Thr	Val	Glu	Trp	
				85					90					95		
AGG	GCA	CAG	TCT	GAG	TCT	GCC	CGG	AGC	AAG							318
Arg	Ala	Gln	Ser	Glu	Ser	Ala	Arg	Ser	Lys							
			100					105								

## (2) INFORMATION FOR SEQ ID NO:113:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Arg	Leu	Glu	Gln	Pro	Asn	Val	Val	Ile	Ser	Leu	Ser	Arg	Thr	Glu	Ala	
1				5					10					15		
Leu	Asn	His	His	Asn	Thr	Leu	Val	Cys	Ser	Val	Thr	Asp	Phe	Tyr	Pro	
			20					25					30			
Ala	Lys	Ile	Lys	Val	Arg	Trp	Phe	Arg	Asn	Gly	Gln	Glu	Glu	Thr	Val	
			35				40					45				
Gly	Val	Ser	Ser	Thr	Gln	Leu	Ile	Arg	Asn	Gly	Asp	Trp	Thr	Phe	Gln	
	50					55					60					
Val	Leu	Val	Met	Leu	Glu	Met	Thr	Pro	Arg	Arg	Gly	Glu	Val	Tyr	Thr	
65					70					75					80	
Cys	His	Val	Glu	His	Pro	Ser	Leu	Lys	Ser	Pro	Ile	Thr	Val	Glu	Trp	
				85					90					95		
Arg	Ala	Gln	Ser	Glu	Ser	Ala	Arg	Ser	Lys							
			100					105								

## (2) INFORMATION FOR SEQ ID NO:114:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: DNA

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1323

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

TTC TTT AAA AAC ATC GTG ACT CCG CGT ACA CCC CCG CCA GGA GGT GGA	48
Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly	
1 5 10 15	
GGC TCT GGA GGT GGA GGC TCA GGA GGA GGT GGG TCC GGA GAC TCC GAA	96
Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Asp Ser Glu	
20 25 30	
AGG CAT TTC GTG TTC CAG TTC AAG GGC GAG TGC TAC TTC ACC AAC GGG	144
Arg His Phe Val Phe Gln Phe Lys Gly Glu Cys Tyr Phe Thr Asn Gly	
35 40 45	
ACG CAG CGC ATA CGA TCT GTG GAC AGA TAC ATC TAC AAC CGG GAG GAG	192
Thr Gln Arg Ile Arg Ser Val Asp Arg Tyr Ile Tyr Asn Arg Glu Glu	
50 55 60	
TAC CTG CGC TTC GAC AGC GAC GTG GGC GAG TAC CGC GCG GTG ACC GAG	240
Tyr Leu Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Glu	
65 70 75 80	
CTG GGG CGG CCA GAC CCC GAG TAC TAC AAT AAG CAG TAC CTG GAG CAA	288
Leu Gly Arg Pro Asp Pro Glu Tyr Tyr Asn Lys Gln Tyr Leu Glu Gln	
85 90 95	
ACG CGG GCC GAG CTG GAC ACG GTG TGC AGA CAC AAC TAC GAG GGG GTG	336
Thr Arg Ala Glu Leu Asp Thr Val Cys Arg His Asn Tyr Glu Gly Val	
100 105 110	
GAG ACC CAC ACC TCC CTG CGG GGT GGA TCA GGT GGC GAA GAC GAC ATT	384
Glu Thr His Thr Ser Leu Arg Gly Gly Ser Gly Gly Glu Asp Asp Ile	
115 120 125	
GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA TAT CAG TCT CCT	432
Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro	
130 135 140	
GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT GAT GAG TGG TTC	480
Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly Asp Glu Trp Phe	
145 150 155 160	
TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG CTT CCT GAG TTT	528
Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met Leu Pro Glu Phe	
165 170 175	
GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG CAA AAC ATA GCT	576
Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala	
180 185 190	
ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG TCA AAT TCC ACC	624
Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr	
195 200 205	
CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT	672
Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe Pro Lys Ser Pro	
210 215 220	
GTG CTG CTG GGT CAG CCC AAA ACC CTT ATC TGC TTT GTG GAC AAC ATC	720
Val Leu Leu Gly Gln Pro Lys Thr Leu Ile Cys Phe Val Asp Asn Ile	
225 230 235 240	



TTC CCT CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC	768
Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn Ser Lys Ser Val	
245 250 255	
ACA GAC GGC GTT TAT GAG ACC AGC TTC CTT GTC AAC CGT GAC CAT TCC	816
Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn Arg Asp His Ser	
260 265 270	
TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT GAC GAT GAT ATT	864
Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile	
275 280 285	
TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA	912
Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Pro Val Leu Lys	
290 295 300	
CAT TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG CTG ACA GAG ACT	960
His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu Leu Thr Glu Thr	
305 310 315 320	
GGC GGA GGT GGC TCA GGC GGA GGT GGA TCT GGA GGT GGA GGC TCA CGG	1008
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg	
325 330 335	
CTT GAA CAG CCC AAT GTC GTC ATC TCC CTG TCC AGG ACA GAG GCC CTC	1056
Leu Glu Gln Pro Asn Val Val Ile Ser Leu Ser Arg Thr Glu Ala Leu	
340 345 350	
AAC CAC CAC AAC ACT CTG GTC TGC TCA GTG ACA GAT TTC TAC CCA GCC	1104
Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro Ala	
355 360 365	
AAG ATC AAA GTG CGC TGG TTC CGG AAT GGC CAG GAG GAG ACG GTG GGG	1152
Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val Gly	
370 375 380	
GTC TCA TCC ACA CAG CTT ATT AGG AAT GGG GAC TGG ACC TTC CAG GTC	1200
Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln Val	
385 390 395 400	
CTG GTC ATG CTG GAG ATG ACC CCT CGG CGG GGA GAG GTC TAC ACC TGC	1248
Leu Val Met Leu Glu Met Thr Pro Arg Arg Gly Glu Val Tyr Thr Cys	
405 410 415	
CAC GTG GAG CAT CCG AGC CTG AAG AGC CCC ATC ACT GTG GAG TGG AGG	1296
His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp Arg	
420 425 430	
GCA CAG TCT GAG TCT GCC CGG AGC AAG	1323
Ala Gln Ser Glu Ser Ala Arg Ser Lys	
435 440	

## (2) INFORMATION FOR SEQ ID NO:115:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEO ID NO:115:

Phe	Phe	Lys	Asn	Ile	Val	Thr	Pro	Arg	Thr	Pro	Pro	Pro	Gly	Gly	Gly
1					5				10					15	
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Asp	Ser	Glu
			20					25					30		
Arg	His	Phe	Val	Phe	Gln	Phe	Lys	Gly	Glu	Cys	Tyr	Phe	Thr	Asn	Gly
		35					40					45			
Thr	Gln	Arg	Ile	Arg	Ser	Val	Asp	Arg	Tyr	Ile	Tyr	Asn	Arg	Glu	Glu
	50					55					60				
Tyr	Leu	Arg	Phe	Asp	Ser	Asp	Val	Gly	Glu	Tyr	Arg	Ala	Val	Thr	Glu
65					70					75					80
Leu	Gly	Arg	Pro	Asp	Pro	Glu	Tyr	Tyr	Asn	Lys	Gln	Tyr	Leu	Glu	Gln
				85					90					95	
Thr	Arg	Ala	Glu	Leu	Asp	Thr	Val	Cys	Arg	His	Asn	Tyr	Glu	Gly	Val
			100					105					110		
Glu	Thr	His	Thr	Ser	Leu	Arg	Gly	Gly	Ser	Gly	Gly	Glu	Asp	Asp	Ile
		115					120					125			
Glu	Ala	Asp	His	Val	Gly	Val	Tyr	Gly	Thr	Thr	Val	Tyr	Gln	Ser	Pro
	130					135					140				
Gly	Asp	Ile	Gly	Gln	Tyr	Thr	His	Glu	Phe	Asp	Gly	Asp	Glu	Trp	Phe
145					150					155					160
Tyr	Val	Asp	Leu	Asp	Lys	Lys	Glu	Thr	Ile	Trp	Met	Leu	Pro	Glu	Phe
				165					170					175	
Gly	Gln	Leu	Thr	Ser	Phe	Asp	Pro	Gln	Gly	Gly	Leu	Gln	Asn	Ile	Ala
			180					185					190		
Thr	Gly	Lys	Tyr	Thr	Leu	Gly	Ile	Leu	Thr	Lys	Arg	Ser	Asn	Ser	Thr
		195					200					205			
Pro	Ala	Thr	Asn	Glu	Ala	Pro	Gln	Ala	Thr	Val	Phe	Pro	Lys	Ser	Pro
	210					215					220				
Val	Leu	Leu	Gly	Gln	Pro	Lys	Thr	Leu	Ile	Cys	Phe	Val	Asp	Asn	Ile
225					230					235					240
Phe	Pro	Pro	Val	Ile	Asn	Ile	Thr	Trp	Leu	Arg	Asn	Ser	Lys	Ser	Val
				245					250					255	
Thr	Asp	Gly	Val	Tyr	Glu	Thr	Ser	Phe	Leu	Val	Asn	Arg	Asp	His	Ser
			260					265					270		
Phe	His	Lys	Leu	Ser	Tyr	Leu	Thr	Phe	Ile	Pro	Ser	Asp	Asp	Asp	Ile
		275					280					285			
Tyr	Asp	Cys	Lys	Val	Glu	His	Trp	Gly	Leu	Glu	Glu	Pro	Val	Leu	Lys
	290					295					300				
His	Trp	Glu	Pro	Glu	Ile	Pro	Ala	Pro	Met	Ser	Glu	Leu	Thr	Glu	Thr
305					310					315					320

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Arg  
                   325                  330                  335  
 Leu Glu Gln Pro Asn Val Val Ile Ser Leu Ser Arg Thr Glu Ala Leu  
                   340                  345                  350  
 Asn His His Asn Thr Leu Val Cys Ser Val Thr Asp Phe Tyr Pro Ala  
                   355                  360                  365  
 Lys Ile Lys Val Arg Trp Phe Arg Asn Gly Gln Glu Glu Thr Val Gly  
                   370                  375                  380  
 Val Ser Ser Thr Gln Leu Ile Arg Asn Gly Asp Trp Thr Phe Gln Val  
                   385                  390                  395                  400  
 Leu Val Met Leu Glu Met Thr Pro Arg Arg Gly Glu Val Tyr Thr Cys  
                   405                  410                  415  
 His Val Glu His Pro Ser Leu Lys Ser Pro Ile Thr Val Glu Trp Arg  
                   420                  425                  430  
 Ala Gln Ser Glu Ser Ala Arg Ser Lys  
                   435                  440

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 588 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..588

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC GTC TAT GGT ACA ACT GTA	48
Glu Asp Asp Ile Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val	
1                  5                  10                  15	
TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC ACA CAT GAA TTT GAT GGT	96
Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly	
20                  25                  30	
GAT GAG TGG TTC TAT GTG GAC TTG GAT AAG AAG GAG ACT ATC TGG ATG	144
Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met	
35                  40                  45	
CTT CCT GAG TTT GGC CAA TTG ACA AGC TTT GAC CCC CAA GGT GGA CTG	192
Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu	
50                  55                  60	

CAA AAC ATA GCT ACA GGA AAA TAC ACC TTG GGA ATC TTG ACT AAG AGG	240
Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg	
65 70 75 80	
TCA AAT TCC ACC CCA GCT ACC AAT GAG GCT CCT CAA GCG ACT GTG TTC	288
Ser Asn Ser Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe	
85 90 95	
CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC AAC ACC CTT ATC TGC TTT	336
Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe	
100 105 110	
GTG GAC AAC ATC TTC CCT CCT GTG ATC AAC ATC ACA TGG CTC AGA AAT	384
Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn	
115 120 125	
AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG ACC AGC TTC CTT GTC AAC	432
Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn	
130 135 140	
CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT CTC ACC TTC ATC CCT TCT	480
Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser	
145 150 155 160	
GAC GAT GAT ATT TAT GAC TGC AAG GTG GAG CAC TGG GGC CTG GAG GAG	528
Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu	
165 170 175	
CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT CCA GCC CCC ATG TCA GAG	576
Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu	
180 185 190	
CTG ACA GAG ACT	588
Leu Thr Glu Thr	
195	

## (2) INFORMATION FOR SEQ ID NO:117:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Glu Asp Asp Ile Glu Ala Asp His Val Gly Val Tyr Gly Thr Thr Val	
1 5 10 15	
Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr Thr His Glu Phe Asp Gly	
20 25 30	
Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys Lys Glu Thr Ile Trp Met	
35 40 45	
Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe Asp Pro Gln Gly Gly Leu	
50 55 60	

Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu Gly Ile Leu Thr Lys Arg  
 65 70 75 80  
 Ser Asn Ser Thr Pro Ala Thr Asn Glu Ala Pro Gln Ala Thr Val Phe  
 85 90 95  
 Pro Lys Ser Pro Val Leu Leu Gly Gln Pro Asn Thr Leu Ile Cys Phe  
 100 105 110  
 Val Asp Asn Ile Phe Pro Pro Val Ile Asn Ile Thr Trp Leu Arg Asn  
 115 120 125  
 Ser Lys Ser Val Thr Asp Gly Val Tyr Glu Thr Ser Phe Leu Val Asn  
 130 135 140  
 Arg Asp His Ser Phe His Lys Leu Ser Tyr Leu Thr Phe Ile Pro Ser  
 145 150 155 160  
 Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu His Trp Gly Leu Glu Glu  
 165 170 175  
 Pro Val Leu Lys His Trp Glu Pro Glu Ile Pro Ala Pro Met Ser Glu  
 180 185 190  
 Leu Thr Glu Thr  
 195

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..702

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

TTC TTT AAA AAC ATC GTG ACT CCG CGT ACA CCC CCG CCA GGA GGT GGA	48
Phe Phe Lys Asn Ile Val Thr Pro Arg Thr Pro Pro Pro Gly Gly Gly	
1 5 10 15	
GGC TCT GGA GGT GGA GGC TCA GGA GGA GGT GGG TCT GGC GGT GGA GGT	96
Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly	
20 25 30	
TCC GGC GGA GGC GGT TCA GAA GAC GAC ATT GAG GCC GAC CAC GTA GGC	144
Ser Gly Gly Gly Gly Ser Glu Asp Asp Ile Glu Ala Asp His Val Gly	
35 40 45	
GTC TAT GGT ACA ACT GTA TAT CAG TCT CCT GGA GAC ATT GGC CAG TAC	192
Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr	
50 55 60	

ACA CAT GAA TTT GAT GGT GAT GAG TGG TTC TAT GTG GAC TTG GAT AAG	240
Thr His Glu Phe Asp Gly Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys	
65 70 75 80	
AAG GAG ACT ATC TGG ATG CTT CCT GAG TTT GGC CAA TTG ACA AGC TTT	288
Lys Glu Thr Ile Trp Met Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe	
85 90 95	
GAC CCC CAA GGT GGA CTG CAA AAC ATA GCT ACA GGA AAA TAC ACC TTG	336
Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu	
100 105 110	
GGA ATC TTG ACT AAG AGG TCA AAT TCC ACC CCA GCT ACC AAT GAG GCT	384
Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr Pro Ala Thr Asn Glu Ala	
115 120 125	
CCT CAA GCG ACT GTG TTC CCC AAG TCC CCT GTG CTG CTG GGT CAG CCC	432
Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln Pro	
130 135 140	
AAC ACC CTT ATC TGC TTT GTG GAC AAC ATC TTC CCT CCT GTG ATC AAC	480
Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile Asn	
145 150 155 160	
ATC ACA TGG CTC AGA AAT AGC AAG TCA GTC ACA GAC GGC GTT TAT GAG	528
Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr Glu	
165 170 175	
ACC AGC TTC CTT GTC AAC CGT GAC CAT TCC TTC CAC AAG CTG TCT TAT	576
Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser Tyr	
180 185 190	
CTC ACC TTC ATC CCT TCT GAC GAT GAT ATT TAT GAC TGC AAG GTG GAG	624
Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu	
195 200 205	
CAC TGG GGC CTG GAG GAG CCG GTT CTG AAA CAC TGG GAA CCT GAG ATT	672
His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu Ile	
210 215 220	
CCA GCC CCC ATG TCA GAG CTG ACA GAG ACT	702
Pro Ala Pro Met Ser Glu Leu Thr Glu Thr	
225 230	

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

Phe	Phe	Lys	Asn	Ile	Val	Thr	Pro	Arg	Thr	Pro	Pro	Pro	Gly	Gly	Gly
1				5				10					15		

Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly  
 20 25 30  
 Ser Gly Gly Gly Gly Ser Glu Asp Asp Ile Glu Ala Asp His Val Gly  
 35 40 45  
 Val Tyr Gly Thr Thr Val Tyr Gln Ser Pro Gly Asp Ile Gly Gln Tyr  
 50 55 60  
 Thr His Glu Phe Asp Gly Asp Glu Trp Phe Tyr Val Asp Leu Asp Lys  
 65 70 75 80  
 Lys Glu Thr Ile Trp Met Leu Pro Glu Phe Gly Gln Leu Thr Ser Phe  
 85 90 95  
 Asp Pro Gln Gly Gly Leu Gln Asn Ile Ala Thr Gly Lys Tyr Thr Leu  
 100 105 110  
 Gly Ile Leu Thr Lys Arg Ser Asn Ser Thr Pro Ala Thr Asn Glu Ala  
 115 120 125  
 Pro Gln Ala Thr Val Phe Pro Lys Ser Pro Val Leu Leu Gly Gln Pro  
 130 135 140  
 Asn Thr Leu Ile Cys Phe Val Asp Asn Ile Phe Pro Pro Val Ile Asn  
 145 150 155 160  
 Ile Thr Trp Leu Arg Asn Ser Lys Ser Val Thr Asp Gly Val Tyr Glu  
 165 170 175  
 Thr Ser Phe Leu Val Asn Arg Asp His Ser Phe His Lys Leu Ser Tyr  
 180 185 190  
 Leu Thr Phe Ile Pro Ser Asp Asp Asp Ile Tyr Asp Cys Lys Val Glu  
 195 200 205  
 His Trp Gly Leu Glu Glu Pro Val Leu Lys His Trp Glu Pro Glu Ile  
 210 215 220  
 Pro Ala Pro Met Ser Glu Leu Thr Glu Thr  
 225 230

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..279

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

GGG GAC ACC CGA CCA CGT TTC CTG TGG CAG CCT AAG AGG GAG TGT CAT 48  
 Gly Asp Thr Arg Pro Arg Phe Leu Trp Gln Pro Lys Arg Glu Cys His  
 1 5 10 15

TTC TTC AAT GGG ACG GAG CGG GTG CGG TTC CTG GAC AGA TAC TTC TAT 96  
 Phe Phe Asn Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr  
 20 25 30

AAC CAG GAG GAG TCC GTG CGC TTC GAC AGC GAC GTG GGG GAG TTC CGG 144  
 Asn Gln Glu Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg  
 35 40 45

GCG GTG ACG GAG CTG GGG CGG CCT GAC GCT GAG TAC TGG AAC AGC CAG 192  
 Ala Val Thr Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln  
 50 55 60

AAG GAC ATC CTG GAG CAG GCG CGG GCC GCG GTG GAC ACC TAC TGC AGA 240  
 Lys Asp Ile Leu Glu Gln Ala Arg Ala Ala Val Asp Thr Tyr Cys Arg  
 65 70 75 80

CAC AAC TAC GGG GTT GTG GAG AGC TTC ACA GTG CAG CGG 279  
 His Asn Tyr Gly Val Glu Ser Phe Thr Val Gln Arg  
 85 90

## (2) INFORMATION FOR SEQ ID NO:121:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Gly Asp Thr Arg Pro Arg Phe Leu Trp Gln Pro Lys Arg Glu Cys His  
 1 5 10 15

Phe Phe Asn Gly Thr Glu Arg Val Arg Phe Leu Asp Arg Tyr Phe Tyr  
 20 25 30

Asn Gln Glu Glu Ser Val Arg Phe Asp Ser Asp Val Gly Glu Phe Arg  
 35 40 45

Ala Val Thr Glu Leu Gly Arg Pro Asp Ala Glu Tyr Trp Asn Ser Gln  
 50 55 60

Lys Asp Ile Leu Glu Gln Ala Arg Ala Ala Val Asp Thr Tyr Cys Arg  
 65 70 75 80

His Asn Tyr Gly Val Val Glu Ser Phe Thr Val Gln Arg  
 85 90